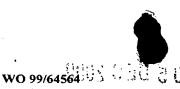


Figure 1. β -Galactosidase phylogenetic tree based on shared amino acid sequence identity. A. Tomato β-galactosidase (TBG) cDNAs. B. Plant β-galactosidases. Higgins-Sharp algorithm (UPGMA method)





Wall av 528 Rec'd PCT/PTO 2 31

Figure 2 Sheet 1 of 12 accession number AF023847; Sequence ID number 1

Gene/clone name: TBG1/pZBG2-1-10; 30 TITTTTCTTTGTTCTTTTTGCTCAGCACTAG 122 214 305 306 ATG GOT TIT TOG ATG GCA ATG TTG CTG ATG TTG TTA TTG TGT TTA TGG GTT TCT TGT GGA ATT GCT TCT 374 1 Met Gly Phe Trp Met Ala Met Leu Leu Met Leu Leu Leu Cys Leu Trp Val Ser Cys Gly Ile Ala Ser 375 GTT TCA TAT GAC CAT AAA GCT ATC ATT GTA AAT GGA CAA AGA AAA ATT CTC ATT TCT GGA TCC ATT CAC 443 24 Val Ser Tyr Asp His Lys Ala Ile Ile Val Asn Gly Gln Arg Lys Ile Leu Ile Ser Gly Ser Ile His 46 444 TAC CCT AGA AGC ACC CCT GAG ATG TGG CCA GAT CTT ATT CAG AAG GCA AAA GAA GGG GGA GTT GAT GTT 512 47 Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Glu Gly Gly Val Asp Val 69 513 ATA CAG ACT TAT GIT TIC TGG AAT GGG CAT GAG CCT GAA GAA GGG AAA TAT TAT TIT GAA GAG AGG TAT 581 70 Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Glu Glu Gly Lys Tyr Phe Glu Glu Arg Tyr 582 GAT TTA GTG AAG TTC ATT AAA GTG GTG CAA GAA GCA GGA CTT TAT GTG CAT CTT AGG ATT GGA CCT TAT 650 93 Asp Leu Val Lys Phe Ile Lys Val Val Gln Glu Ala Gly Leu Tyr Val His Leu Arg Ile Gly Pro Tyr 115 651 GCA TOT GCT GAA TOG AAT TIT GOG GGT TIT CCT GTT TOG CTG AAG TAT GTT CCA GGT ATT AGT TIC AGA 719 116 Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg 138 720 ACA AAC AAT GAG CCA TTC AAG GCT GCA ATG CAA AAG TTC ACT AAG ATT GTT GAT ATG AAA GCA 139 Thr Asn Asn Glu Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Thr Lys Ile Val Asp Met Met Lys Ala 161 789 GAA AAG CTC TAT GAA ACT CAG GGT GGT CCA ATT ATT CTA TCT CAG ATA GAA AAT GAA TAT GGA CCT ATG 857 162 Glu Lys Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Pro Met 184 858 GAG TGG GAA CTA GGT GAA CCT GGT AAA GTT TAC TCA GAA TGG GCA GCC AAA ATG GCT GTG GAT CTT GGC 926 185 Glu Trp Glu Leu Gly Glu Pro Gly Lys Val Tyr Ser Glu Trp Ala Ala Lys Met Ala Val Asp Leu Gly 207 927 ACT GGT GTC CCA TGG ATC ATG TGC AAG CAA GAT GAT GTC CCT GAT CCT ATT ATT AAT ACT TGC AAT GGT 995 208 Thr Gly Val Pro Trp Ile Met Cys Lys Gln Asp Asp Val Pro Asp Pro Ile Ile Asn Thr Cys Asn Gly 996 TTC TAC TGT GAC TAC TTC ACA CCA AAT AAG GCT AAT AAA CCC AAG ATG TGG ACT GAA GCC TGG ACA GCC 1064 231 Phe Tyr Cys Asp Tyr Phe Thr Pro Asn Lys Ala Asn Lys Pro Lys Met Trp Thr Glu Ala Trp Thr Ala 253 1065 TGG TTT ACC GAA TTT GGA GGT CCA GTT CCT TAC CGT CCT GCA GAG GAT ATG GCA TTT GCT GTC GCA AGA 1133 254 Trp Phe Thr Glu Phe Gly Gly Pro Val Pro Tyr Arg Pro Ala Glu Asp Met Ala Phe Ala Val Ala Arg 276 1134 TIT ATA CAA ACG GGA GGC TCC TTC ATC AAT TAC TAT ATG TAT CAT GGA GGA ACA AAC TIT GGA AGG ACT 1202 277 Phe Ile Gln Thr Gly Gly Ser Phe Ile Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr 1203 TCT GGT GGC CCA TIT ATT GCT ACT TAT GAT TAT GAT GCA CCC CTA GAT GAA TIT GGG TCA TTA CGG 1271 300 Ser Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Phe Gly Ser Leu Arg 322 1272 CAG CCT AAA TGG GGT CAT CTG AAA GAT CTA CAT AGA GCA ATA AAG CTC TGT GAG CCA GCT TTA GTA TCT 1340 323 Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Arg Ala Ile Lys Leu Cys Glu Pro Ala Leu Val Ser 345 1341 GTA GAT CCA ACT GTG ACA TCC TTA GGA AAC TAT CAA GAG GCA CGT GTT TTC AAG TCA GAG TCT GGG GCC 1409 346 Val Asp Pro Thr Val Thr Ser Leu Gly Asn Tyr Gln Glu Ala Arg Val Phe Lys Ser Glu Ser Gly Ala 368 1410 TGC GCT GCC TTC CTA GCA AAT TAC AAC CAG CAC TCT TTT GCT AAA GTG GCA TTT GGG AAC ATG CAT TAT 1478 369 Cys Ala Ala Phe Leu Ala Asn Tyr Asn Gln His Ser Phe Ala Lys Val Ala Phe Gly Asn Met His Tyr 391 1547 1479 AAC TTG CCA CCC TGG TCT ATC AGC ATT CTT CCC GAC TGC AAG AAC ACT GTC TAT AAT ACT GCA AGG GTT 392 Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Asn Thr Val Tyr Asn Thr Ala Arg Val 1548 GGT GCT CAA AGT GCT CAG ATG AAG ATG ACT CCA GTC AGT AGA GGA TTC TCA TGG GAG TCA TTC AAT GAA 1616 415 Gly Ala Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly Phe Ser Trp Glu Ser Phe Asn Glu 437





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	Sh et 20112	AF023847;	Securities	ID	number	1	cont.

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430	Asp	ALG	A10	Jer				•																
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461	ger:	Ual Ual	COT	Aen	TVY	TTG Leu	Tro	Tyr	Met	Thr	Asp	Ile	Glu	Ile	Asp	Pro	Thr	Glu	Gly	Phe	Leu	ASN	ser	483
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1755	CCA	ጥልል	TYCC:	CT.	TGG	CTT	ACT	GTC	Lalal	TCT	GCT	GGC	CAT	GCA	TTG	CAT	GTA	TTC	CTC	AAT	GGT	CAA	TTA	1823
1/33	Clu	ver	TTT	Pro	Tim	Leu	Thr	Val	Phe	Ser	Ala	Gly	His	Ala	Leu	His	Val	Phe	Val	Asn	GIA	GIN	Leu	506
404	Gry	A311	110																				~~	1892
1824	CCA	CCA	ΔСТ	GTG	TAC	GGA	AGT	TTA	GAA	AAC	CCA	AAA	CTA	ACT	TTC	AGC	AAC	CCT	ATA	AAT	CIG	AGA	GCT	529
2024	מוג	Glv	Thr	Val	TVT	GGA Gly	Ser	Leu	Glu	Asn	Pro	Lys	Leu	Thr	Phe	Ser	Asn	Gly	Ile	Asn	Leu	Arg	AIA	323
507	MIG	Gry	****	142	-3-	,																		1961
1893	CCT	CITC	AAC	AAG	ATT	TCT	CTG	CTA	AGC	ATT	GCT	GTT	GGT	CTT	ccc	AAC	GIT	GGC	CCT	CAT	Lil.	GAG	ALA	552
1033	Cly	Val	Asn	INS	Ile	Ser	Leu	Leu	Ser	Ile	Ala	Val	Gly	Leu	Pro	Asn	Val	Gly	Pro	His	Pne	GIU	Thi	332
530	GIY	Vul																						2030
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552	100	Acn.	AIA	Glv	Val	Leu	Gly	Pro	Val	Ser	Leu	Asn	Gly	Leu	Asn	Glu	Gly	Thr	Arg	Asp	Leu	THE	TTP	373
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2031	CAG	AAA	TGG	TTC	TAC	AAG	GTT	GGT	CTA	AAA	GGA	GAA	CCC	CIG	AGT	CIT	CAT	TCA	CIC	AGT	GGT	AUC	CCA.	598
576	Gln	INS	THE	Phe	TVI	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ala	Leu	Ser	Leu	His	Ser	Leu	ser	GIY	ser	PIO	2,0
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2100	TY.	CTC	GAG	TGG	GTG	GAA	GGC	TCT	TTA	GTG	CCT	CAG	aag	CAG	CCA	CIC	AGT	TGG	TAT	AAG	ACT	MLA.	Dho	621
500	Car	Val	Glu	TID	Val	GAA	Gly	Ser	Leu	Val	Ala	Gln	Lys	Gln	Pro	Leu	Ser	Trp	Tyr	Lys	THE	1111	FILE	021
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622	yen	Ala	Pro	Asp	Glv	Asn	Glu	Pro	Leu	Ala	Leu	Asp	Met	Asn	Thr	Met	Gly	Lys	GIA	GIN	VAI	TTP	116	044
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2238	AAT	GGT	CAG	AGC	CTC	GGA	CGC	CAC	TGG	CCT	GCA	TAT	AAA	TCA	TCT	GGA	AGT	TGT	AGT	GIC	761	AAC	TAL.	667
645	Asn	Glv	Gln	Ser	Leu	GLY	Arg	His	Trp	Pro	Ala	Tyr	Lys	Ser	Ser	Gly	Ser	Cys	Ser	Val	Cys	ASII	ıyı	σσ.
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2307	ACT	GGC	TGG	TTT	GAT	GAG	AAA	AAG	TGC	CTA	ACT	AAC	TGT	GGT	GAG	GGC	TCA	CAA	ALA	100	The	His	Val	690
668	Thr	Glv	Tro	Phe	Asp	GAG	Lys	Lys	Cys	Leu	Thr	Asn	Cys	Gly	Glu	Gly	Ser	Gin	Arg	TTP	ıyı	шэ	V	
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2376	ccc	CGG	TCT	TGG	CTG	TAT	CCT	ACT	GGA	AAT	TTG	TTA	GIT	GTA	TIC	نكاكن	GAA	700	Clu	Gly	Acr	Pro	TAT	713
691	Pro	Arg	Ser	Trp	Leu	Tyr	Pro	Thr	Gly	Asn	Leu	Leu	Val	Val	Pne	GIU	Giu	ııp	GLY	0- 3			Tyr	•
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2445	GGA	ATC	ACT	ATT '	GTC	: AAA	. AGA	GAA	ATA	GGG	AGT	GIT	TGT	GC1	GAI	TIA	Time	Glu	Tre	Gln	Pro	Gln	TTA Leu	736
714	Gly	Ile	Thr	Leu	Val	. Lys	Arg	Glu	Ile	Gly	Ser	Val	cys	ATA	, MS	116	Lyr	014					Leu	
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2514	TTG	TAA	TGG	CAG	AGG	CTA	GTA	TCI	GGI	AAG	TTT	GAC	AGA:	CCI	LIC	. Ava	Pro	LAS	Ala	His	Lev	Lys	TGT Cys	759
737	Leu	Asn	TI	Glr	Arg	Leu	Val	Ser	Gly	Lys	Pne	ASP	Arg	PIC	Dec			-,-					Cys	
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2583	GCA	CCI	GC1	CAC	AAG	TEA	TCI	TCA	ATC	AAA	. 111		Cor	Dhe	GIV	Thr	Pro	Glu	Gly	/ Val	Cys	Gly	AAC Asn	782
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Figure 2 She t3 of 12 Gene/clone name: TBG2/pZBG2-1-12; accession number AF154420; Sequence ID number 2

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3 1	AGC Ser	AGA Arg	AGA Arg	AAA Lys	ACA Thr	Leu	ASD	Phe	Pro	Leu	Ile	Leu	Thr	Val	Leu	Thr	Ile	His	Phe	Val	Ile	Val	Ala	23
72	œc	GAG	. · ТАТ	TTC	AAG	ccc	TTC	AAT	GTC	ACC	TAC	GAT	AAC	CGA	GCT	CIC	ATC	ATC	GGC	GGT	AAA	œc	CGT	140
24	Gly	Glu	Тут	Phe	Lys	Pro	Phe	Asn	Val	Thr	Tyr	Asp	Asn	Arg	Ala	Deu	116	116	Gry	GIY	Lys	AL Y	AL Y	46
141	ATG	CTT	ATC	TCC	GCC	GGA	ATT	CAC	TAC	CCT	CCC	GCC	ACT,	CCT	GAG	ATG	TGG	ccc	ACA	TTG	ATA	GCT	AGG	209 69
47	Met	Leu	Ile	Ser	Ala	Gly	Ile	His	Тут	Pro	Arg	Ala	Thr	Pro	GIU	Met	чтр	PIO	ти	Deu	116	Ala	ALY	69
210	AGC	AAA	GAA	GGT	GGT	GCA	GAT	GTC	ATC	GAG	ACT	TAT	ACA	TTT	TGG	TAA	GGT	CAT	GAG	CCA	ACC Thr	AGG Ara	GGA	278 92
					Gly																			
279	CAG	TAC	AAT	TTT	GAA	GGA	AGA	TAT	GAT	ATT	GTC	AAG	TTC	GCA	AAG	CTA	GTC Val	GGA	TCT	CAT	GGA	Leu	Phe	347 115
					Glu																			
348	CTC	TTT	TTA	CGA	ATA Ile	GGT	CCT	TAT	GCC	TGT	GCA	GAA	TGG	AAC	TTC	GGG	GGA	TTC	Pro	ATA	TCG	CTT	Arg	416 138
																								405
417	GAT	ATA	CCT	GGA	ATA Ile	GAA	TTT	CGA	ACA	GAT	TAA	GCA	CCA	TTC	AAG	GAG	GAG	ATG	GAG Glu	OGC Ara	TAT	GTT Val	Lys	485 161
486	AAG	ATA	GTT	GAT	CTT	atg	ATA	TCT	GAG	TCG	CTC	TTT	TCG	TGG	CAA	GGT	GGT	CCT	ATC	ATT	TTG	CTG Leu	CAG Gln	· 554 184
					Leu																			
555	TTA	GAA	AAT	GAA	TAT	GGA	AAT	GTT	GAA	AGC	TCA	TTC	GGT	CCC	AAG	GGG	AAG	TTA	TAT TVT	ATG Met	AAA Lvs	TCG	GCT Ala	623 207
					Tyr																			600
624	CT	GAA	ATG	GCT	GIT	GGT	CTT	GGT	GCT	GGT	GTT	CCA	TGG	GTC	ATG	TGC	AGG	CAA	ACT	GAT	GCT Ala	CCA Pro	GAA Glu	692 230
					Val																			761
693	TAC	ATC	ATA	GAT	ACT	TGT	AAT	GCA	TAC	TAT	TGT	GAT	GGG	TTC	ACG	CCG	AAT	TCC	GAG	AAG	LVS	Pro	Lvs	761 253
					Thr																			070
762	ATT	TGG	ACT	GAG	AAT	TGG	AAT	GGA	TGG	TTT	GCA	GAT	TGG	GGT	GAA	AGA	CTT	CCA	TAT	AGA Ara	Pro	TCC	GAG Glu	830 276
					Asn																			000
831	GAT	ATT	GCA	TTT	GCA	TTA	GCT	CGT	TTC	TTT	CAA	CGT	GGG	GGC	AGC	TTA	CAG	AAC	TAT	TAT	ATG	TAT	TTT Phe	899 299
					Ala																			0.00
900	GGT	GGG	ACA	TAA	TTT	GGC	CGG	ACT	GCT	GGT	GGC	CCA	ACT	CAA	ATC	ACT	AGC	TAT	GAT	TAT	GAT	GCT	Pro	968 322
					Phe																			
969	CTG	GAT	GAA	TAT	GGA	CTA	CTA	CGT	CAA	CCT	AAA	TGG	GGC	CAT	TTG	AAG	GAT	CTG	CAT	GCT Ala	GCT	ATA Ile	AAG Lvs	1037 345
					Gly																			
1038	CTT	TGT	GAA	CCA	GCT	CTT	GTT	GCT	GCT	GAT	TCA	CCT	CAG	TAT	ATT	AAA	CTG	GGA	CCA	AAA	CAG Gln	GAG Glu	GCA Ala	1106 368
					Ala																			
1107	CAT	GTC	TAT	CGT	GGA	ACA	TCC	AAC	AAC	ATT	GGC	CAA	TAT	ATG	TCC	TTA	AAT	GAA	GGC	ATA	TGC C∨s	GCA Ala	GCA Ala	1175 391
					Gly																			
1176	TTT	ATT	GCA	LAAT	TTA	GAT	GAA	CAT	GAA	TCA	GCA	ACA	GIG	AAA	TTT	TAC	COT	CAA	GAG	TTC	ACT	TTA Leu	Pro	1244 414
392	Phe	Ile	Ala	Asn	Ile	Asp	Glu	His	Glu	Ser	Ala	Thr	Val	Lys	Pne	Tyr	GIY	GIN	Giu	rne				
1245	CCA	TGG	TCA	GTG	GTA	TTC	TGC	CAG	ATT	GCA	GAA	ATA	CAG	CTT	TCA	ACA	CAG	CTA	AGG	TGG	GGG	CAC	LVS	1313 437
415	Pro	Trp	Ser	Val	Val	Phe	Cys	Gln	Ile	Ala	Glu	He	Gin	Leu	Ser	THE	GIN	Leu	Arg	11p	017		_,_	
1314	CTT	CAA	TCA	AAA	CAG	TGG	GCT	CAG	ATT	CTG	TTT	CAG	TTG	GGA	ATA	ATT	CTT	TGT	TTC	TAC	AAG	TTA	TCA	1382 460
438	Leu	Ģln	Ser	Lys	Gln	Trp	Ala	Gln	Ile	Lėu	Phe	Gln	Leu	Gly	Ile	Ile	Leu	cys	Pue	ıyr	Lys	Deu	J-51	-





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1383 461	CTA Leu	AAA Lys	GCA Ala	AGC Ser	TCG Ser	GAA Glu	AGT Ser	TTT Phe	TCA Ser	CAA Gln	TCT Ser	TGG Trp	ATG Met	ACA Thr	TTG Leu	AAG Lys	GAG	Pro	Leu	Gly	Val	Trp	Gly	483	
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1452 484	GAC	AAG	TAA	TTC	ACT	TCT	AAA	GUA	Tie	Leu	Glu	His	Leu	Asn	Val	Thr	Lys	Asp	Gln	Ser	Asp	Tyr	Leu	506	
484	Asp	Lys	ASN	Pne	7111	261	Dy 5	02,												~~m	C-UAIL	»	~~	1589	
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1659	AAA	GGC	AAA	TGG	ATC	AAG	GTG	CTT	CAA	CCI	GIT	AAG	CTG	GTT	CAG	GGA	TVT	Asn	ASD	Ile	Leu	Leu	Lev	575	
553	Lys	Gly	Lys	Trp	Ile	Lys	Vai	vaı	GIII	FIU	701	_,													
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1728	TCT	GAG	ACG	Ual	GGA	TTG Leu	Gln	Àsn	Tyr	Gly	Ala	Phe	Leu	Glu	Lys	Asp	Gly	Ala	Gly	Phe	Lys	.Gly	Glr	598	ì
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1797	ATA	AAG	CTT	ACA	GGA	TGC	AAA	AGC	GGG	GAT	ATC	TAA	CTC	ACA	ACA	Ser	Leu	TTD	Thr	Tyr	Gln	Val	Gly	621	i
599.	Ile	Lys	Leu	Thr	Gly	Cys	Lys	Ser	GIY	App															
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1866	CTT	AGA	GGC	GAA	Phe	CTG Leu	Glu	Val	Tyr	Asp	Val	Asn	Ser	Thr	Glu	Ser	Ala	Gly	Trp	Thr	Glu	Phe	Pro	644	,
622	Leu	AL 9														C N IT	ccc	~~	ccc	ccc	ACA	GAT	ccz	2003	3
1935	ACT	GGT	ACA	ACT	CCG	TCA	GTC	LLL	TCG	TGG	TAC	AAG	ACA	AAG	Phe	ASD	Ala	Pro	Gly	Gly	Thr	Asp	Pro	667	7
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691	Trp	Thr	Leu	Val	Ala	PTO	ASII	ASII	GIŞ	Cys	<b>01</b> 3	5		•										A 221	n
2142	444	TY2T	AGG	: ACA	AAC	TGT	GGA	GAG	ATT	ACT	CAG	ĞCC	TGG	TAC	CAT	ATA	CCT	AGA	TCA	TGG	CTA	INS	Th	73	
714	Lys	Cys	Arg	Thr	Asn	Cys	Gly	Glu	Ile	Thr	Gln	Ala	Trp	Tyr	His	He	PTO	Arg	Ser	111	, 200	_,_			
												~~~		N/T	ന്നു	dalal.	GAT	ATT	TCC	ATI	TCI	ACG	CC	r 227	
2211	TTA	raa .	AAT	GTA	CTA	GTT Val	ATC	Phe	GAA	Glu	Thr	Asp	Lys	Thr	Pro	Phe	Asp	Ile	Ser	: Ile	: Ser	Thr	Ar	g 75	9
737	Lev	AST	ASI	ı vaı	Leu	Val	110	1110				-										C 2 T	· m^	G 234	8
2280	101	AC1	GAZ	A ACC	TTA:	TGI	GCT	CAA	GTA	TCG	GAA	AAG	CAC	TAT	CCA	CCI	CTA	CAT	LAK	TYT	Ser	His	. Se	r 78	
760) Sex	Thi	: Gl:	ı Thi	: Ile	cys	. Ala	GII	Val	361	GIU			- •											
													~~>	CAA	ΔTC	CAC	TTG	CAG	TG	r GAC	GAZ	. GG≱	CA	T 241	
2349	GAG	TT	r GAG	CAG	A AAC	TTC Lev	Ser	Lev	Met	Asp	Lys	Thr	Pro	Glu	Met	His	Leu	Gln	Cys	Ası	o Glu	G13	/ Hi	s 80	2
783	9 611	1 Pile	: A5	h wri	, 2,	,				_									2.20	- गग	- 4702	CAZ	A GG	A 248	6
2418	B AC	TA A	TC	T TC	r at	r GA/	TT	CC	AGC	TAT	GG/	AGT	CCG	TAA	GGC	AGC	. IGI	Gln	LV	s Pho	e Sei	Gli	ı Gl	y 82	
806	5 Th	r Il	e Se	r Se	r Ile	e GI	1 Pne	S WIG	, ser	191	01)				_										
														. ~~	4477	י אדו	GGA	AGA	AC	r ag	r TG	: AGC	TA C	T 255	
248	/ AA	A TG	CA	r GC	A Al	A AAT	. ici	Let	Ser	Val	Va.	Ser	Glr	Ala	Cys	; Ile	: Gly	Arg	Th	r Se	r Cys	s Se	r Il	.e 85	1.1
82	, Lly	- Су	s ni	. AI									_				. ,,,,,,	. 4414		יייט יו	T CA	A GC	A AA	A 262	24
255	6 GG	C AT	T TC	C AA	T GG	r GT	A TT	r GG/	A GAT	CC	TG	r CGA	CAC	GIT	UP	AAL LVS	Ser	Lev	Al	a Va	1 Gl	n Al	a Ly	's 87	14
85	2 Gl	y Il	e Se	r As	n Gl	y Va.	1 Ph	e GT	y ASL	PLC	, cy.	, me	,			_									
262		~ ~~	. ~	·» cc	» ~~	A GA	~ ~ TY	- AG	ac?	TC	\ GC	r TCC	TCC	TGF	GG	AGAC"	rctgo	TAAC	ACG	AATT	CCTT	PAG.	AACC	AA 270)2 38
262 27	o TG	C TC	A CC	A CC	o Pr	o As	p Le	u Se:	r Thi	Sei	Ala	s Sei	Sei	•••	•										, 0
67	. cy	. <i>.</i> e			- • •	,							 -		~~~	MT	~ 200~	ימידים	יי ם בי	CAGG	CGGA	GAAA	ACG7	TAC 279	94
270	3 AC	GATC	CCTI	DAAA	TCCA	CTCG AAAT	TTCC	CCTG	cccc	GAG	CCT	CTGC1	raca?	L'L'IC'	ATCT TOTAL	IGCT	CATGO	CATA	GAG	CTGC	TAAA	TATA	TGAC	AA 28	
279	5 AT	GGAC	GATT	TTAC	TIGI	TAAA AAAA	TTTA TTTA	GGTT.	ACTG!	ATA'	LAAA LATT	MATT	CAAC	ACCA:	rtta'	TAA	AAGT	ragt	raac	AZYA	TTAA	AAAA	AAA	AAA 291	
		OAAT: 4AAA		KAAA	ATAG	MMAA	CICC	.010																291	74
431	, n		•																						

Gene/clone name: TBG3/p2-

0c/bl;

Figure 2
She t5 of 12
accession number AF154421; Selence ID number 3

1 31	aagj	\GGA/	LAAA!	\ATA/	\AGT¶	AAA!	GGGC(;ccc]	Laaaj	AGTT!	PTCA!	PPTTC	CCTI	KAAA:	AGGC	AGJ (ACA)	GTTC LTCTI	ATTA GATA	TTTT GAAF	TTTT AGGF	GCATA GATA	TTTC	TAC	30 121
						:			TYPE:	דע ג	CTG	TTG	TTG	GTG	TIG	TTG	GGT	TCA	TGG	GTT	TTT	TCT	GGA	190
122	ATG	GGT	TGT	ACG	CTT	ATA	CIA	Mer	Leu	Asn	Val	Leu	Leu	Val	Leu	Leu	Gly	Ser	Trp	Val	Phe	Ser	Gly	23
1	Met	Gly	Cys	rnr	Leu	116	Dea	Mec		•							-							
101	NCN.	CO-TT	т~т	הער	TCA	TAT	GAC	CAT	AGG	GCT	ATT	ATT	GTA	TAA	GGA	CAA	AGA	AGA	ATA	CTT	ATT	TCT	GGT	259
191	Thr	Ala	Ser	Val	Ser	Tyr	Asp	His	Arg	Ala	Ile	Ile	Val	Asn	Gly	Gln	Arg	Arg	Ile	Leu	He	Ser	GIA	46
24	****					-													~~	222	GAD	422	CCT	328
260	TCT	GTT	CAT	TAT	CCA	AGA	AGC	ACT	CCT	GAG	ATG	TGG	CCA	GCT	ATT	ATT	CAA	AAG	Ala	INS	Glu	Glv	Glv	69
47	Ser	Val	His	Tyr	Pro	Arg	Ser	Thr	Pro	Glu	Met	Trp	PTO	GIY	116	116	GIII	Lys	VI.C.	2,0		,		
										m~~	እእጥ	CCA	СУТ	GAG	CCT	CAA	CAA	GGG	AAA	TAT	TAT	TTT	GAA	397
329	CIC	GAT	GIG	TTA	CAG	ACT	TAT	GTT.	Phe	TTD	Asn	Gly	His	Glu	Pro	Gln	Gln	Gly	Lys	Tyr	Tyr	Phe	Glu	92
70	Val	Asp	Val	He	GIn	1111	171	407																
200	~~	AC A	ጥልጥ	GAT	TTA	GTG	AAG	TTT	ATT	AAG	CTG	GTG	CAC	CAA	GCA	GGA	CTT	TAT	GIC	CAT	CTT	AGA	GTT	466 115
390	Clv	Ara	Tvr	Asp	Leu	Val	Lys	Phe	Ile	Lys	Leu	Val	His	Gln	Ala	Gly	Leu	ŢYI	Val	His	Leu	Arg	vai	115
,,,	U23	9	-,-														~~~		ጥአጥ	ست	CCA	CCT	ATC	535
. 467	GGA	CCT	TAT	GCT	TGT	CCT	GAA	TGG	AAT	Lili	GGG	GGC	TTT	CCT	GIT	TGG	Lou	LAAA	TAI	Val	Pro	Gly	Ile	138
116	Gly	Pro	Tyr	Ala	Cys	Ala	Glu	Trp	Asn	Phe	GIY	Gly	Pne	PIO	vai	Trp	Leu	цуз	.,.	•				
										***	~	CCA	MTC	CA A	444	Jalak	ACT	GCC	AAG	ATT	GTC	TAA	ATG	604
536	AGT	TIC	AGA	ACA	GAT	AAT	Clar	CCI	Phe	LVS	Ala	Ala	Met	Gln	Lys	Phe	Thr	Ala	Lys	Ile	Val	Asn	Met	161
139	Ser	Phe	Arg	Thr	Asp	ASII	GIY	-10		_,_					_									600
605	NTC	***	ccc	GAA	CCT	TTG	TAT	GAA	ACT	CAA	GGG	GGG	CCA	ATA	ATT	TTA	TCT	CAG	ATT	GAG	TAA	GAA	TAT	673 184
162	Mer	Lvs	Ala	Glu	Arg	Leu	Tyr	Glu	Thr	Gln	Gly	Gly	Pro	Ile	Ile	Leu	Ser	Gln	Ile	Glu	Asn	GIU	Tyr	104
102																		~~~		444	ATY:	CCT	GTG	742
674	GGA	ccc	ATG	GAA	TGG	GAA	CIG	GGA	GCA	CCA	GGT	AAA	TCT	TAC	GCA Nla	CAG	100 Trm	Δla	Ala	Lvs	Met	Ala	Val	207
185	Gly	Pro	Met	Glu	Trp	Glu	Leu	GIY	ATA	PIO	GIY	Буз	Jer							-				
											m-c	NAC.	CAA	CAC	таэ	GCC	CCT	GAT	CCT	ATT	ATA	AAT	GCT	811
743	GGT	CTT	GAC	ACT	GGT	GIC	Dro	100	Val	Met	Cvs	Lys	Gln	Asp	Asp	Ala	Pro	Asp	Pro	Ile	Ile	Asn	Ala	230
208	Gly	Leu	Asp	Thr	GIY	vai	PIO					_		_										880
012	mcc.	* እእጥ	GGC	- Janes	TAC	TGT	GAC	TAC	LLL	TCT	CCA	AAC	aag	CCT	TAT	AAA	CCA	AAG	ATA	TGG	ACT	GAA	GCC	253
231	CVS	Asn	Glv	Phe	Tyr	Cys	Asp	Tyr	Phe	Ser	Pro	Asn	Lys	Ala	Tyr	Lys	Pro	Lys	Ile	arp	The	GIU	Ala	233
	,-	-			-	_									~~	~~	~~	CNG	GAC	JAIL!	GCA	TTT	TCT	949
881	TGG	ACT	GCA	TGG	TTT	ACT	GGT	LLL	GGA	AAT	CCA	GTT V=1	CCT	TAC	CGI	Dro	A J P	Chu	Asp	Leu	Ala	Phe	Ser	276
254	Trp	Thr	Ala	Trp	Phe	Thr	GIA	Pne	GIY	ASII	FIO	VAI	110	• , -					_					
								~~~	CCT	•	- Tel	ATC	аат	TAT	TAC	ATG	TAT	CAT	GGA	GGA	ACA	AAC	TTT	1018
950	GIT	GC#	, AA	' Jala	ATA	CAG	TAR	C) v	Glv	Ser	Phe	Ile	Asn	Tyr	Tyr	Met	Тут	His	Gly	Gly	Thr	Asn	Phe	<b>29</b> 9
277	Val	Ala	Lys	Pne	tre	GIII	LDys	02,	,					-										1007
1016		. ~	: A~	י ככיו	GGT	GGT	CCA	TTI	ATT	GCT	ACT	AGT	TAT	GAC	TAT	GAT	GCA	CCA	CIL	GAT	GAA	TAT	Cly	1087 322
300	G	Arc	Thi	Ala	Gly	Gly	Pro	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	GIU	туг	GIY	322
30.	,		,		_													220	باملت	тст	GAA	CCA	GCT	1156
108	TT	TTC	CG/	A CA	CCA	AAA .	TGG	GGT	CAC	CIG	AAA	GAT	CIG	CAT	AUA	Ala	TIA	LVS	Leu	CVS	Glu	Pro	GCT	345
32	Le	Leu	Arg	g Glr	Pro	Lys	Trp	Gly	His	Leu	Lys	Asp	Leu	nis	Arg	VIG	110	2,0					Ala	
								. ~~~		CC3		422	CAC	CAG	CAG	GAG	GCC	CAT	GTI	TTT	AGG	TCG	<b>AA</b> G	1225
115	7 <b>TT</b> /	A GTY	TC	r GG/	A GAT	CCA	. Bla	Ual	Thr	Ala	Leu	Glv	His	Gln	Gln	Glu	Ala	His	Val	Phe	Arg	Ser	Lys	368
34	5 Let	u Va.	ı se	r G13	/ AST	PIC	, 410																	1204
122	s cc	T (20)		ייאר יו	י ככיו	r GC#	TTC	CTI	GCT	AAC	TAC	GAC	CAA	CAC	TCT	TIT	GCT	ACT	GIG	TCA	Jalai	GC	AAC Asn	1294 391
36	O GC.	a Gl	v Se:	r Cv	s Ala	Ala	Phe	Lev	Ala	Asn	тут	Asp	Gln	His	Ser	Phe	Ala	Thr	Val	Sex	Pne	. Ale	Asn	371
50			,	,															- x~1	י כידי	لملمك	י אמי	ACA 1	1363
129	5 AG	G CA	T TA	C AA	C TIC	CCI	A CC	TGG	TC	ATC	AGC	ATT	CIT	CCC	GAC	160	LAG	AAC	Thr	· Val	Phe	Asr	ACA Thr	414
39	2 Ar	g Hi	s Ту	r Ası	n Lei	ı Pro	Pro	) LIF	Ser	: Ile	e Ser	Ile	Leu	Pro	ASP	, cys	Lys	r.sii	:				Thr	
												. nor	л <b>~</b> т	~~	CTY	· AGC	AGA	GGA	TTC	ccc	TGC	CAC	TCA	1432
136	4 GC	A CG	G AT	c cc	r GC	r CA	A AGT	ו שלים - רא	CAC	, MIC	INC	Met	Thr	Pro	Val	Ser	Arg	Gly	Leu	Pro	Tr	Gli	Ser	437
41	5 Al	a Ar	g Il	e Gl	A VI	ננט פ	, sei	. 410	. 311		,-						_	_						1501
142		~ »	ጥ ርኦ	A GA	G AC	A TC	A TCT	r TAT	r GAJ	GAC	AG1	AGT	Lalal	ACA	GTI	. CILI	. eec	CTA	TTC	GA/	CAC	AT/	A AAT e Asn	1501 460
143	אם ט יניני ר	L MA	n G1	11 GA	u Thi	r Se	r Sei	тут	Gli	ı Asr	Ser	Ser	Phe	Thr	Val	Va1	Gly	Leu	Leu	ı Glu	) G11	111	e Asn	400
43	O FII		51	. 01				-		_														





## 528 Rec'd POTATIED NO STUED 2006

PCT/US99/12697

Figure 2
She t6 of 12
a name: TBG3/p2-1-3 bl; accession number AF154421; Sequence ID stumber 3 cont.

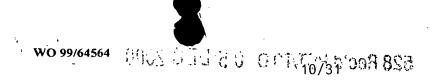
1502	202	404	AGA	GAC	ങ്ങ	TCT	GAT	TAT	TTG	TGG	TAT	TCA	ACA	GAT	GTC	aag	ATT	GAT	TCA	AGA	GAA	AAG	Jalal	1570
1502 461	Thr	Thr	Ara	Asp	Val	Ser	Asp	Tyr	Leu	Trp	Тут	Ser	Thr	Asp	Val	Lys	Ile	Asp	Ser	Arg	Glu	Lys	Phe	483
																								1639
1571	TTG	AGA	GGC	GGA	AAA	TGG	CCT	TGG	CIL	ACG	ATC	ATG	TCA	GCT	GGG	CAT	GCA	116	UAI	VAI	Phe	Val	Asn	506
1571 484	Leu -	Arg	Gly	Gly	Lys	Trp	Pro	Trp	Leu	Thr	Ile	Met	Ser	Ala	GIA	HIS	AIA	Leu	nis	441		***		300
1640			• • •								entro.	CAA	444	ന്നു	AAA	CTA	ACT	TTC	AGT	AAA	ĠCC	GTA	AAT	1708
1640 507	GCT	CAA	TTA	GCA	GGA	ACT	GCA	TAT	Ch	Cor	Len	Glu	Lvs	Pro	Lvs	Leu	Thr	Phe	Ser	Lys	Ala	Val	Asn	529
507	Gly	Gln	Leu	ATA	GIY	THE	AIU	IYI	GIY		<b>D</b> C.0		-,-		•									
1709	CTC	424	CCA	CCT	Calar	AAC	AAG	TTA	TCT	CTA	CTG	AGC	ATT	GCT	GTT	GGC	CTT	CCG	AAT	ATC	GGC	CCA	CAT	1777
1709 530	Len	Ara	Ala	Glv	Val	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Ile	Ala	Val	Gly	Leu	Pro	Asn	Ile	Gly	Pro	His	552
																								1846
1778	TTT	GAG	ACA	TGG	TAA	GCT	CCT	GII	CIT	GGG	CCA	GIC	TCA	CTA	ACT	COL	Low	ACD	Chr	GIV	LVS	Arg	ASD	575
1778 553	Phe	Glu	Thr	Trp	Asn	Ala	Gly	Val	Leu	Gly	Pro	Vai	Ser	Leu	1111	GIY	Deu	ىرجىر	020	02,	-,-		•	
1847								m> C	8 8 C	CTT	CCT	СТА	AAA	GGA	GAA	GCC	TTG	AGC	CTC	CAT	TCA	CTC	AGT	1915
1847 576	TTA	ACA	TGG	CAG	AAA	100	Ser	TVT	INS	Val	Gly	Leu	Lys	Gly	Glu	Ala	Leu	Ser	Leu	His	Ser	Leu	Ser	598
																								1984
1916	CCT	AGC	TCG	TCA	GTT	GAG	TGG	GTC	GAG	GGT	TCT	TTA	GTG	CCI	CAG	AGA	CAG	CCA	CIC	ACA	TGG	TAC	AAG	621
599	Gly	Ser	Ser	Ser	Val	Glu	Trp	Val	Glu	Gly	Ser	Leu	Val	Ala	Gln	Arg	Gln	Pro	Leu	Thr	urp	ıyı	пåг	021
																								. 2053
1985	AGC	ACT	TTT	AAT	GCT	CCA	GCT Ala	GGA	AAT	GAT	CCI	TIG	Ala	Len	ASD	Leu	Asn	Thr	Met	Gly	Lys	Gly	Gln	644
2054	~~~		202	2.20	CCT	CAA	AGC	CTC	GGA	CGC	TAT	TGG	ССТ	GGA.	TAT	AAA	GCA	TCT	GGT	AAC	TGC	GGT	GCC	2122
645	Val	Tim	Tle	Asn	Glv	Gln	Ser	Leu	Gly	Arg	Tyr	Trp	Pro	Gly	Tyr	Lys	Ala	Ser	Gly	Asn	Cys	Gly	Ala	667 .
																								2191
2123	TGT	AAC	TAT	GCA	GGC	TGG	TTT	AAT	GAG	AAA	AAA	TGC	CTA	AGT	AAC	TGT	GGA	GAG	Ala	Ser	Gln	Arg	Tro	690
668	Cys	Asn	Tyr	Ala	Gly	Trp	Phe	Asn	Glu	Lys	Lys	Cys	Leu	ser	Asn	Cys	GIA	GIU	Ala	561	· · ·	,		
2192		_						~~~	mam.	~~	المال	GGA	AAT	TIG	TTA	GTT	CTA	TTT	GAG	GAA	TGG	GGA	GGA	2260
2192	TAT	CAT	GTT	CCC	CGT	TCI	Trp	ten	TVT	Pro	Thr	Glv	Asn	Leu	Leu	Val	Leu	Phe	Glu	Glu	Trp	Gly	Gly	713
																								2329
2261	GAG	CCT	CAT	GGA	ATC	TCT	TTG	GTA	AAA	AGA	GAA	GTT	GCA	AGT	GTT	TGT	GCA	GAT	ATA	AAC	GAA	TGG	CAA	736
714	Glu	Pro	His	Gly	Ile	Ser	Leu	Val	Lys	Arg	Glu	Val	Ala	Ser	Val	Cys	Ala	Asp	He	Asn	GIU	пр	GIII	,,,,
																								2398
2330	CCA	CAG	TTG	GIG	AAT	TGG	Gln	ATG	CAA	GCA	TCT	GGT	TAR	Val	Asp	Lvs	Pro	Leu	Arg	Pro	Lys	Ala	His	759
2399	~~~	m~	m~n	CCT	· 11/-11	CCT	CAG	AAG	ATT	ACT	TCA	ATC	AAA	TTT	GCA	AGC	TIT	GGA	ACA	CCA	CAA	GGG	GIC	2467
760	Leu	Ser	CVS	Ala	Ser	Glv	Gln	Lys	Ile	Thr	Ser	Ile	Lys	Phe	Ala	Ser	Phe	Gly	Thr	Pro	Gln	Gly	Val	782
																								2536
2468	TGC	GGA	AGC	TTC	CGI	GAA	GGA	AGC	TGC	CAC	GCC	TTC	CAC	TCA	TAT	GAT	GCT	The	GAA	Arg	TVY	CVS	Ile	805
783	Cys	Gly	Ser	Phe	. Arg	Glu	Gly	Ser	Cys	His	Ala	Phe	His	ser	тут	Asp	Ala	Pile	GIU	, muy	- , -	-,-	Ile	
2537							~~~	~	~~~	202	~~	GAG	ATC	JalaL	GGA	GGT	GAT	CCA	TGT	CCA	CAT	GIT	ATG	2605
2537	GGG	CAA	AAC	TO	TGC	CON	. GIA	Dro	Val	Thr	Pro	Glu	Ile	Phe	Gly	Gly	Asp	Pro	Cys	Pro	His	Val	Met	828
																								2000
2606	AAG	AAA	CTC	TC	GTI	GAG	GTI	ATT	TGC	AGT	TGA	TGA	CACT	GAGG	AGAA	ACAA	AATA	AAGT	GGTT	TCAG	TTAG	TIGI	CTGA	2686 840
829	Lys	Lys	Lev	. Sei	· Val	Glu	Val	Ile	Cys	Ser	***													
													~-	~~~	,,,,,,,,,	<b>√~ № «төт</b>	ance successive	രവ	ТАТА	СААТ	TGC	ATGG	CCCA	2778
2687	CAT	ATC	LAAAJ	CTT	GCT	TGAT	GGAC	GTG	AGTT	GTAC	AGAT	ATGC	AACA N N N M	CTAN	7.1.1C	CTAC	ATAT	GTCA	TTGG	TTCA	AGTO	CGCA	CCCA	2870
																							TCGAC SAAAG SAAAS	
2871	ATT	GIGG	TAGT	rGGG/	NGGTV	CIAC	PCIAC PCIAC	יבעראי. רבעראי	COAL	TATA	TGTT	ACTG	TTGG	AATT	TGCA	AATC	TIGI	GATT	TCAG	CAAA	<b>LAAA</b> .	AAAA.	<b>KAAA</b> A	3054
3055						*W1 11	~~~																	3069
2023		- uu v			-																			

1								LAAA	<b>NAAA</b>	TTT	CAAT!	rrrr.	rric:	LAAAT	LAATA	AAAA	AAAT.	CAT.	rrrr.	MAG	LATG	roga.	AAA	63
4						~~~	TTG	date:	TT'A	44th	· CTT	АТТ	TGT	TTA	TIG	GAT	TTT	TTT	TCT	TCA	GTG	AAA	GCT	132
64	Mar	CTA	Ara	Thr	AAT	Val	Leu	Leu	Leu	Leu	Val	Ile	Cys	Leu	Leu	Asp	Phe	Phe	Ser	Ser	Val	Lys	Ala	23
133	AGT	GIT	TCT	TAT	GAT	GAC	AGA	GCT	ATA	ATC	ATA	AAT	GGG	AAA	AGA	AAA	ATT	CTT	ATT	TCT	Clv	TCA	ATT	201 46
24	Ser	Val	Ser	Tyr	<b>Asp</b>	Asp	Arg	Ala	Ile	Ile	Ile	Asn	Gly	Lys	Arg	ьуs	116	Leu	TIE	Ser	GIY	·	116	40
							CCA	~~	N 0770	mac	~	CAT	بلملم	ATA	CAA	AAG	GCT	AAA	GAT	GGA	GGC	TTA	GAT	270
202	CAT	TAT	CCA	AGA	AGC	ACT	Pro	Gln	Met	Tro	Pro	Asp	Leu	lle	Gln	Lys	Ala	Lys	Asp	Gly	Gly	Leu	Asp	69
271	GTT	TTA	GAA	ACT	TAT	GTT	TTC	TGG	AAT	GGA	CAT	GAG	CCT	TCT	CCT	GGA	AAA	TAT	AAT	TTT	GAA	GGA	AGA	339 92
70	Val	Ile	Glu	Thr	Tyr	Val	Phe	Trp	Asn	Gly	His	Glu	Pro	Ser	Pro	Gly	Lys	тут	ASN	Pne	GIU	GIY	ΑĽĠ	72
			•				ATC			~~~	<b>~</b>	202	CC3	CCA	بلملت	тат	GIC	AAT	TTA	CGT	ATT	GGC	CCT	408
340	TAT	GAT	CTT	GTT	AGA	TTC	Ile	AAA	Mot	Ual	Gln	Ara	Ala	Gly	Leu	Tyr	Val	Asn	Leu	Arg	Ile	Gly	Pro	115
409	TAC	GTC	TGT	GCT	GAA	TGG	AAC	TTT	GGG	GGA	TTC	CCT	GTT	<b>TG</b> G	CTA	AAA	TAT	GTG	CCI	GGT	ATG	GAA	JAT	477
116	Tyr	Val	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Phe	Pro	Val	Trp	Leu	Lys	Tyr	Val	PTO	GIA	Met	GIU	Pne	138
																								546
478	AGA	ACA	AAC	AAT	CAG	CCT	TTT Phe	AAG	GIG	GCT Ala	Mot	Gln	Giv	Phe	Val	Gln	Lvs	Ile	Val	Asn	Met	Met	Lys	161
547	4.7E	GA2)	ААТ	শশভ	JalaL	GAA	TCT	CAA	GGA	GGA	CCA	ATA	TTA	ATG	GCC	CAG	ATA	GAA	TAA	GAG	TAT	GGA	CCA	615
162	Ser	Glu	Asn	Leu	Phe	Glu	Ser	Gln	Gly	Gly	Pro	Ile	Ile	Met	Ala	Gln	Ile	Glu	Asn	Glu	Tyr	Gly	Pro	184
																								684
616	GTA	GAA	TGG	GAA	ATT	GGT	GCT	CCT	GGT	AAA	GCT	TAT	ACA mbx	AAA	100	Ala	Ala	Gln	Met	Ala	Val	Gly	Leu	207
							Ala																	
605		»CT	CCT	C-TV-	~~	TYC:	ATC	ATG	тст	AAG	CAA	GAG	GAT	GCT	CCT	GAT	CCT	GTG	TTA	GAT	ACT	TGT	TAA	753
208	LVS	Thr	Glv	Val	Pro	Tro	Ile	Met	Cys	Lys	Gln	Glu	Asp	Ala	Pro	Asp	Pro	Val	Ile	Asp	Thr	Cys	Asn	230
																								822
754	GGC	TTC	TAC	TGC	GAA	GGG	TTC	CGT	CCT	AAT	AAG	CCT	TAC	AAA	CCT	AAA	Mot	100	Thr	Glu	Val	Tro	Thr	253
231	Gly	Phe	Tyr	Cys	Glu	Gly	Phe	Arg	Pro	Asn	Lys	Pro	ıyı	Lys	PIO	Dys	THE	110						
022	~~	arcs:	ጥልጥ	MC	222	TY	GGT	GGT	CCA	ATT	CCT	CAA	AGA	CCA	GCC	GAA	GAC	ATT	GCA	TTT	TCA	GTT	GCC	891
254	Glv	Tro	Tvr	Thr	Lvs	Phe	Gly	Gly	Pro	Ile	Pro	Gln	Arg	Pro	Ala	Glu	Asp	Ile	Ala	Phe	Ser	Val	Ala	276
																								960
892	AGG	TTT	GTT	CAG	AAC	AAT	GGT	TCA	TTC	TTC	AAT	TAC	TAC	ATG	TAT	CAT	GUA	COA	Thr	Asn	Phe	Glv	Arg	299
277	Arg	Phe	Val	. Gln	Asn	Asn	Gly	Ser	Phe	Phe	Asn	тут	туг	met	Tyr	ura	Gry	O.,						
063		<b>~</b>	<b>m</b> 0.1	~~	~mm	mm·	ATT	CC.	аст	AGC	TAC	GAT	TAT	GAT	GCT	CCT	CTC	GAT	GAA	TAT	GGG	TTG	CIG	1029
300	Thr	Ser	Ser	Glv	Len	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	qzA	Glu	Tyr	Gly	Leu	Leu	322
																								1098
1030	AAT	GAA	CCA	AAG	TAT	GGG	CAC	TIG	AGA	GAC	TTA	CAT	AAA	GCT	ATC	AAG	CTA	TCT	GAA	Pro	GCT	TAU	Val	345
323	Asn	Glu	Pro	Lys	Tyr	Gly	His	Leu	Arg	Asp	Leu	His	Lys	Ala	11e	Lys	Leu	Ser	GIU	FIO	ALU			
1099						~~~	N (70)	»		CCA	тод	TAA	CAA	GAG	GCT	CAT	GTT	TAT	AGA	TCA	AAA	TCT	GGA	1167
1099	TCA	COT	TAT	GCT	Ala	טנט ומע	Thr	Ser	Leu	Glv	Ser	Asn	Gln	Glu	Ala	His	Val	Tyr	Arg	Ser	Lys	Ser	Gly	368
																								1236
1168	GCT	TGT	GCT	GCT	TIT	TTA	TCC	AAC	TAT	GAC	TCT	AGA	TAT	TCA	GTA	AAA	CLC	ACC	TIT	CAG	AAT	AGG	Dro	391
369	Ala	Cys	Ala	Ala	Phe	Leu	Ser	Asn	Tyr	Asp	Ser	Arg	Tyr	Ser	Val	Lys	Vai	Thr	Pne	GIN	ASII	ALG	FIO	332
							TCC																	1305
1237	TAC	TAA	CIG	CCI	CCA	TGG	Ser	ATC	Ser	Tle	Leu	Pro	Asp	Cys	Lys	Thr	Ala	Val	Tyr	Asn	Thr	Ala	Gln	414
1306	GTI	AAC	TCT	CAA	AGC	TCG	AGC	ATA	AAG	ATG	ACG	CCT	GCA	GGT	CCT	GGA	TTG	TCT	TGG	CAG	TCA	TAC	AAT	1374 437
415	Val	Asr	Ser	Glr	Ser	Ser	Ser	Ile	Lys	Met	Thr	Pro	Ala	GЉ	ÇĮÀ	Gly	Leu	Ser	Trp	Gln	ser	ıyr	ASI	431
																								1443
1375	GAA	GAA	ACC	CCI	AC1	GCT	GAT Asp	GAC	AGC	GAT	ACA	Lev	Thr	Ala	Asn	Gly	Leu	Trp	Glu	Gln	Lys	Asn	Val	460
438	Glu	Glu	Thr	Pro	Thr	Ala	ASP	MSP	ser	veb	1111	₽Eu				-,		•			-			• •





														12			Figure 2 Sheet 8 of 12 ne/clone name: TBG4/pZBG2-1011/pTomβgal4; accession number AF0203 sequence ID number 4														
e/cl	200	nas	10:	TBG	4/p	ZBG2	-	l/pī	omb	<b>7a14</b>					umbe	K T	F02	33	9 8	eque	nce	ID	num	per 4							
.,								-																cont							
1444	ACA	AGA	GAT	TCA	TCA	GAC	TAT	CTG	TGG	TAC	ATG	ACA	AAT	GTA	AAT	ATA	GCA	TCT	AAT	GAA	GGA	TTT	CTA	151							
461	Thr	Arg	Asp	Ser	Ser	Asp	Tyr	Leu	Trp	Tyr	Met	Thr	Asn	Val	Asn	Ile	Ala	Ser	Asn	Glu	Gly	Phe	Leu	48							
1513	AAG	AAC	GGA	AAG	GAT	ССТ	TAT	CTC	ACT	GTT	ATG	TCC	GCT	GGT	CAT	GTC	TTG	CAT	GTT	TTC	GTC	AAT	GGA	158							
484	Lys	Asn	Gly	Lys	Asp	Pro	Tyr	Leu	Thr	Val	Met	Ser	Ala	Gly	His	Val	Leu	His	Val	Phe	Val	Asn	Gly	50							
1582	AAA	СТА	TCA	GGA	ACT	GTT	TAT	GGT	ACA	TTG	GAT	TAA	CCA	AAA	CTT	ACA	TAC	AGT	GGC	AAC	.ĠTG	AAG	TTA	165							
507	Lys	Leu	Ser	Gly	Thr	Val	Тух	Gly	Thr	Leu	Asp	Asn	Pro	Lys	Leu	Thr	Tyr	Ser	Gly	Asn	Val	Lys	Leu	52							
1651	AGA	GCT	GGT	ATT	AAC	AAG	ATT	TCT	CTG	CTC	AGT	GTT	TCC	GTT	GGT	CTC	CCG	AAC	GTT	GGC	GTG	CAT	TAT	171							
530	Arg	Ala	Gly	Ile	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Val	Ser	Val	Gly	Leu	Pro	Asn	Val	Gly	Val	His	Tyr	55:							
1720	GAT	ACA	TGG	AAT	GCA	GGA	GTT	CTA	GCT	CCA	GTC	ACG	TTG	AGC	CCT	CTC	AAT	GAA	GGG	TCA	AGA	AAC	TTG	178							
553	Asp	Thr	Trp	Asn	Ala	Cly	Val	Leu	Gly	Pro	Val	Thr	Leu	Ser	Gly	Leu	Asn	Glu	Gly	Ser	Arg	Asn	Leu	57!							
1789	GCG	AAA	CAG	AAA	TGG	TCT	TAC	AAG	GTT	GGT	CTG	AAA	GGC	GAA	TCG	TTA	AGT	CTT	CAC	TCC	TTA	agt	GGG	185							
576	Ala	Lys	Gln	Lys	Trp	Ser	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ser	Leu	Ser	Leu	His	Ser	Leu	Ser	Gly	598							
1858	AGT	TCT	TCT	GTT	GAA	TGG	GTT	CGA	GGT	TCA	CTA	ATG	GCT	CAA	AAG	CAG	œc	CTG	ACT	TGG	TAC	AAG	CCT	1926							
599	Ser	Ser	Ser	Val	Glu	Trp	Val	Arg	GJA	Ser	Leu	Met	Ala	Gln	Lys	Gln	Pro	Leu	Thr	Trp	Tyr	Lys	Ala	621							
1927	ACA	TTT	AAC	GCG	ССТ	GGA	GGA	AAT	GAT	CCA	CTA	GCT	ATT	GAC	ATG	GCA	AGT	ATG	GGA	AAA	GCT	CAG	ATA ·	1999							
622	Thr	Phe	Asn	Ala	Pro	Gly	Gly	Asn	Asp	Pro	Leu	Ala	Leu	Asp	Met	Ala	Ser	Met	Gly	Lys	Gly	Gln	Ile	644							
1996	TGG	ATA	TAA	GGT	GAA	GGC	GTA	GGT	CGC	CAT	TGG	CCT	GGA	TAC	ATA	GCA	CAA	GGC	GAC	TGC	AGC	AAA	TGC	2064							
645	Trp	Ile	Asn	Gly	Glu	Gly	Val	Gly	Arg	His	Trp	Pro	Gly	Tyr	Ile	Ala	Gln	Gly	Asp	Cys	Ser	Lys	Cys	667							
2065	AGT	TAT	GCT	GGA	ACG	TTC	AAC	GAG	AAG	AAG	TGC	CAG	ACT	AAC	TGC	GGA	CAA	ССТ	TCT	CAG	AGA	TGG	TAC	2133							
668	Ser	Tyr	Ala	Gly	Thr	Phe	Asn	Glu	Lys	Lys	Cys	Gln	Thr	Asn	Cys	Gly	Gln	Pro	Ser	Gln	Arg	Trp	Тут	690							
2134	CAT	GTT	CCA	CGA	TCG	TGG	CTG	AAA	CCA	AGT	GGA	AAC	TTG	TTA	GTA .	GTA	TTC	GAA	GAA	TGG	GGA	GGT	AAT	2202							
691	His	Val	Pro	Arg	Ser	Trp	Leu	Lys	Pro	Ser	Gly	Asn	Leu	Leu	Val	Val	Phe	Glu	Glu	Trp	Gly	Gly	Asn	713							
2203	CCA	ACA	GGA	ATT	TCT	CTA	GTC	AGG	AGA	TCA	<b>A</b> GA	AAT	AGA	CTC	<b>SAAA</b> E	GTA	aaci	TGT	CAG:	PAACT	ATGG	TCCI	TGAA	2282							
714	Pro	Thr	Gly	Ile	Ser	Leu	Val	Arg	Arg	Ser	Arg	***												725							
2283	TTO	GCGC(	CGAA	AAAT	ACATA	ACACO	AAGO	TAAC	AATC	GAGO	CTAC	AGT	TGC	LAAT?	IGCAC	CTG	ATA	AAC	TTAC	SAAGA	AAAT.	GAAA	TTAT	2374							
2375	TGA	TAA!	AAGG	ACTA	LATA	TTA	CACAC	SAGA	TTTI	CTT	YTTA!	TTT	<b>TAA</b> T	ACT	MGGT	TTAT	'AAAC	TTT	TAC	AGAA?	ALLIC	TGT	TTTA	2466							





09/701868

PCT/US99/12697

Figure 2 Sh t 9 of 12

Gene/clone name: TBG5/RT R2-1/bl; accession number AF154423; Sequence ID number 5

1	ATC	CAG	ACT	TAC	GIT	TTC	TGG	AAC	CIT	CAT	GAA	CCI	GIT	CGA	. AAT	CAG	TAT	CAT.	J-I-I.	GAA	GGA	7433	AAA	0:
1	Tle	Gln	Thr	Tyr	Val	Phe	Tro	Asn	Leu	His	Glu	Pro	Val	Arg	Asn	Gln	Tyr	Asp	Phe	Glu	Gly	Arg	Lys	23
70	CAT	JAZZ.	ልጥ	. ልልጥ	- Andah	CTC	AAG	TTG	GTG	GAG	AGA	GCT	GGC	TTA	LLL	GTT	CAT	ATA	AGG	ATT	GGG	CCT	TAT	138
. 74	OW.	Lau	710	, vvv	Dho	Val	TAKS	Leu	Val	Glu	Arg	Ala	Gly	Leu	Phe	Val	His	Ile	Arg	Ile	Ğly	Pro	Tyr	46
24	MS _L	Deu	116	ASII	FILE	VUI	-,-				_		•						-					
120	CONT	an Sala	CCA	CAA	TYCE	220	ሞልጥ	CCT	GGG	TTT	CCT	CTT	TGG	TTG	CAT	TTC	ATT	CCT	GGA	ATT	GAA	TTT	CGA	207
47	1751	0	Ala elk	Clu	700	Asn	Tur	Glv	Glv	Phe	Pro	Leu	Trp	Leu	His	Phe	Ile	Pro	Gly	Ile	Glu	Phe	Arg	69
• '	AGI	Cys	A14	GIU	ILP	<i>A</i> D4.	• , -	<b>-</b> -,	,				, ,											
200	300	CNC	вът	CAA	core.	-Atrib	DAG	GCA	GAA	ATG	AAG	CGA	TTC	ACA	GCT	AAA	ATT	GTT	GAC	ATG	ATC	AAG	CAA	276
70	Mary.	yez	ver	Glu	Dro	Phe	LVS	Ala	Glu	Met	Lvs	Arg	Phe	Thr	Ala	Lys	Ile	Val	Asp	Met	Ile	Lув	Gln	92
		طحا	<i>-</i> L3.1	<b>514</b>							-	_				_								
77	CNA	ייית	CTD A	ጥአጥ	GC»	TCC	CAG	GCT	GGG	œ	GTT	ATC	TTG	TCT	CAG	ATA	GAA	AAT	GAG	TAT	GGC	AAT	GGT	345
03	Ghi	Aen	LAN	There	Ala	Ser	Gln	Glv	Glv	Pro	Val	Ile	Leu	Ser	Gln	Ile	Glu	Asn	Glu	Tyr	Gly	Asn	Gly	115
"	GIU			- 3 -	****			,																
146	CAT	אדים	GAG	ىلمكال	ىرى	TAT	GGT	CCT	CGT	GCC	AAA	CCT	TAC	GTG	AAC	TGG	GCA	GCA	TCA	ATG	CCT	ACG	TCT	414
116	Am	Tle	Glu	Cor	ATO	Tyr	Glv	Pro	Arg	Ala	Lys	Pro	Tyr	Val	Asn	Trp	Ala	Ala	Ser	Met	Ala	Thr	Ser	138
115	A.L.	TAA	λCC	422	CELLO:	CCA	TGG	GTT	ATG	TGT	CAG	CAA	CCA	GAT	GCC	CCT	CCI	TCC	GIT	TTA	AAC	ACT	TGC	483
39	Len	Asn	Thr	Glv	Val	Pro	Tro	Val	Met	Суз	Gln	Gln	Pro	Asp	Ala	Pro	Pro	Ser	Val	Ile	neA	Thr	Cys	161
184	ААТ	GGA	Jalal	тат	TGT	GAC	CAA	TTC	AAG	CAA	AAT	TCC	GAT	AAA	ACA	$\infty$	AAG	ATG.	TGG	ACT	GAG	AAT	<b>TG</b> G	552
62	Asn	Glv	Phe	Tvr	CVS	Asp	Gln	Phe	Lys	Gln	<b>As</b> n	Ser	q <b>z</b> £	Lys	Thr	Pro	Lys	Met	Trp	Thr	Glu	Asn	Trp	184
553	ACC	GGA	TGG	Jelel	CTG	TCG	TIT	GGT	GGT	CCT	CIC	CCT	TAC	AGA	CCA	GTG	GAA	GAC	ATC	CCT	TTC	CCT	GIG	621
85	Thr	Glv	Tro	Phe	Leu	Ser	Phe	Gly	Gly	Pro	Val	Pro	Tyr	Arg	Pro	Val	Glu	Asp	Ile	Ala	Phe	Ala	Val	207
22	CCT	CGA	TTT.	TTC	CAG	CGA	GGC	GGA	ACT	TTC	CAG	AAC	TAT	TAC	ATG	TAC	CAC	GGG	GGA	ACT	AAC	TTT	GGG	690
108	λla	Ara	Phe	Phe	Gln	Arg	Gly	Gly	Thr	Phe	Gln	maA	Tyr	Tyr	Met	Tyr	His	Gly	Gly	The	Asn	Phe	Gly	230
91	AGA	ACC	AGT	GGT	GGA	CCG	TTT	ATT	GCA	ACT	AGC	TAT	GAC	TAT	GAT	GCC.	CCT	CTC	GAC	GAA	TAC	<b>G</b> G		755
231	Aro	Thr	Ser	Gly	Gly	Pro	Phe	Ϊle	Ala	Thr	Ser	Тут	Asp	Tyr	<b>QzA</b>	Ala	Pro	Leu	Asp	Glu	Tyr			252



WO 99/64564



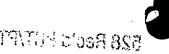
## 09/701868

PCT/US99/12697

11/31

Figure 2
Sheet 10 of 12
Gene/clone name: TBG6/RT R2-6/bl; accession number AF154424; Tuence 7D number 5

•	***	CNC	202	m s m	~	COLLAI.	TYCE:	TAA	Lite	CAT	GAG	CCT	TCT	CCT	تخاف	WWI	IMC	WWI	111	Carr.	000		****	•
T	AIC	CAG	MLA	TWI	GIT		100		17-1	wie	Glu	Dro	Car	Pro	Glv	Asn	TVY	Asn	Phe	Glu	Gly	Arg	Tyr	2
1	Ile	Gln	Thr	Tyr	Val	Phe	TTP	ASI	VAI	UTS	Gru	FIU	<u>م</u>		<b></b> 3		-,-				•	_	-	
														~~~	m> m	~~	~»~	CALAL	CC)	ратег	CCC	CT	ቸልር	13
70	GAC	CTG	GTG	AGG	TIT	GTA	AAA	ACG	ATT	CAG	AAA	GCA	GGG	CIG	TAT	GCT	CAT	CTT	CGA None	TIO	2014	Dra	The sec	4
24	Asp	Leu	Val	Arg	Phe	Val	Lys	Thr	Ile	Gln	Lys	Ala	Gly	Leu	тух	Ala	HIS	Leu	Arg	116	.GIY	FIU	TAT	*
139	GTT	TGT	GCA	GAG	TGG	TAA	TTT	GGA	GGG	TIT	CCA	GTA	TGG	CLC	AAG	TAT	GTA	CCT	CCC	ATT	AGC	TTC	AGA	20
47	Va l	CVS	Ala	Glu	Tro	Asn	Phe	Gly	Gly	Phe	Pro	Val	Trp	Leu	Lys	Tyr	Val	Pro	Gly	Ile	Ser	Phe	Arg	6
		~~~		C	~	and.	AAG	244	GCA	ATC	AAA	GGG	TAT	GCT	GAG	AAA	ATT	GTT	AAC	TIG	ATG	AAG	ATC	27
802	GCT	GAT	AAT	GAA	CC1	Dho	Lvc	Acn	Ala	Met	TAYS	Glv	TVI	Ala	Glu	Lys	Ile	Val	Asn	Leu	Met	Lys	Ile	9:
70	YTS	Asp	ASII	GIU	PIO	PHE	Dys	no	Au	1100	2,0	2				_								
									~~~	~~~	~~~	mac.	and an	CAC	424	TYTE	AGA	ATG	AGT	ATG	GGC	CTC	AAG	34
277	ATA	ATC	Jalal	TCG	AGT	CTC	AGG	GIG	GIC	CAA	TCA	TAL	2	Wi o	2	Ton	720	Met	Ser	Met	Glv	Leu	INS	11
93	Ile	Ile	Phe	Ser	Ser	Leu	Arg	Val	Val	Gin	ser	TYE	Ser	urz	ALG	Dea	AL 9	Met	561		01,		_,_	
						•															Cam	mmc.	220	41
346	CCA	AGG	TAC	TTG	GAG	CAC	ccc	GAC	ATC	AGT	TTA	CAA	CAT	GGG	CIG	CAA	ATA	TGG	عمت	116	GAI	110	AAC	13
116	Pro	Arq	Tyr	Leu	Glu	His	Arg	Asp	Ile	Ser	Ile	Gln	His	Gly	Leu	Gln	Ile	Trp	GIn	Leu	Asp	Leu	ASII	13
116	NCN.	ccc	CTY	422	7000	GTG	ATG	TGC	AAG	GAA	GAA	GAT	GCA	CCA	GAT	CCT	GIG	ATC	AAC	ACA	TGC	AAT	CCT	48
120	W	Clv	Ua?	Dro	420	Val	Met	Cvs	Lvs	Glu	Glu	Asp	Ala	Pro	Asp	Pro	Val	Ile	Asn	Thr	Cys	Asn	Gly	16
133	1111	Gry	Vai	110					3			-												
				~~~			eran.	~~	220	444	420	TAC	AAA	CCT	GCA	ATT	TGG	ACT	GAA	GCT	TGG	AGT	GGA	55
184	TTC	TAC	TGT	GAT	AAT	TIC	TIC	~~	AAC	7	Dro.	Tarr	Lars	Pro	Ala	Tle	Tiro	Thr	Glu	Ala	Trp	Ser	Gly	18
162	Phe	TYT	Cys	Asp	Asn	Pne	Pne	PIO	ASII	пÀ2	PLO	ıyı	2,5								-		_	
													~~1	~~~	CNC	CAT	dals.	CCA	datab	COT	CTT	GCC	CAA	62
553	TGG	TTC.	TCG	GAA	JJJ	GGC	CCT	ccc	CLL	CAT	CAG	ALEA.	-CCA	GII	21-	GA1	7.00	GCA	Dho	Ala	Val	Ala	Gln	20
185	Trp	Phe	Ser	Glu	Phe	Gly	Gly	Pro	Leu	His	Gln	Arg	Pro	Vai	GIII	ASP	Leu	Ala	FIIC	~~~	Vai	****	<b></b> -	
																					~~	~~	NOTE:	69
522	TTT	ATA	CAA	AGA	GGA	GGA	TCT	TIT	GTT	AAC	TAT	TAC	ATG	TAC	CAT	GGG	GGC	ACG	AAC	777	GGA	2000	Wr.	23
208	Phe	Ile	Gln	Arg	Gly	Gly	Ser	Phe	Val	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Pne	GIY	Arg	TILL	23
591	ccc	CCT	GGG	CCA	TTC	ATC	ACT	ACC	AGC	TAT	GAT	TAT	GAT	GCC.	$\alpha$	CIC	GAC	GAG	TAT	GG				74
771	310	Clv	Gly	Dro	Phe	Tle	Thr	Thr	Ser	TVF	ASD	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr					25



12/31

PCT/US99/12697

Figure 2
Sheet 11 of 12
accession number AF154422;

WO 99/64564

																				(	GCAA(	CTIC	rces 4	- <u>r</u> 2
1 13	GTG/	ATA/	ACAC	CGT	AAAC	3GCC	aatg	CAA	CTCT	CCTO	GGAA	TCTG	ATA	GTGA'	TTTA	AGCA	GCTT	AGCT.	AGCT	AACT!	PTTG	CTC	TGCA	103
104	ATG	AAC	ACA	ATG	AGT	TGT	TTG	TCC	TCT	AAT	TTC	AAG	TTC	GTT	TTC	CTT	GCC	TCG	ACT	GTG	ATA	TGG	ATG	172
1	Met	Asn	Thr	Met	Ser	Cys	Leu	Ser	Ser	Asn	Phe	Lys	Phe	Val	Phe	Leu	Ala	Ser	Thr	Val	116	пр	met	23
173	ACG	GTA	ATG	TCG	TCG	TCG	TTA	GCA	GCA	GTA	GAT	GCT	TCC	AAT	GTT	ACT	ACT	ATT	GGT	ACT	GAT	AGT	GTG	241
24	Thr	Val	Met	Ser	Ser	Ser	Leu	Ala	Ala	Val	Asp	Ala	Ser	Asn	Val	Thr	Thr	Ile	Gly	Thr	Asp	Ser	Val	46
242	₽~Т	TAC	GAT	CGA	CGC	TCG	TTG	ATT	ATT	AAC	GGC	CAG	AGG	AAG	CTG	CTC	ATC	TCC	CCT	TCC	ATT	CAC	TAT	310
47	Thr	Tyr	Asp	Arg	Arg	Ser	Leu	Ile	Ile	Asn	Gly	Gln	Arg	Lys	Leu	Leu	Ile	Ser	Ala	Ser	Ile	His	Tyr	69
211	~~T	œc	ACT.	CTC.	ccr	CCC	ATG	TGG	CCT	GGT	CTG	GTT	CGA	TTG	GCG	AAG	GAA	GGA	GGA	GTG	GAT	GTT	TTA	379
70	Pro	Arg	Ser	Val	Pro	Ala	Met	Trp	Pro	Gly	Leu	Val	Arg	Leu	Ala	Lys	Glu	Gly	Gly	Val	Asp	Val'	Ile	92
			<b></b>	~~~	·····	<b>~~</b>	***	CCT	CAC	GAA	CCT	тст	CCG	GGC	AAT	TAT	TAC	TTT.	GGA	A.DD	AGG	TT	GAT	448
93	GAA	Thr	Tyr	Val	Phe	Trp	Asn	Gly	His	Glu	Pro	Ser	Pro	Gly	Asn	Tyr	Tyr	Phe	Gly	Gly	Arg	Phe	Asp	115
					TGT																			517
116	Leu	GTC Val	LVS	Phe	Cys	Lys	Ile	Ile	Gln	Gln	Ala	Gly	Met	Tyr	Met	Ile	Leu	Arg	Ile	Gļy	Pro	Phe	Val	138
																								<b>58</b> 6
518	GCT	GCA	GAA	TGG	AAC Asn	TTT	GGT	GGA	Leu	Pro	Val	Trp	Leu	His	Tyr	Val	Pro	Gly	Thr	Thr	Phe	Arg	Thr	161
																								655
587	GAT	AGT	GAA	CCA	TTT Phe	AAG	TAT	CAC	ATG	CAG Gln	AAG LVS	TTC Phe	ATG Met	ACA	TAT	Thr	Val	Asn	Leu	Met	Lys	Arg	Glu	184
																								724
656	AGG	CTT	TTT	GCA	TCT Ser	CAA	GGA	GGT	CCA	ATC	ATC	TTG	TCA	CAG	GTA Val	GAA	AAT	GAG	TAC	GCC	TVI	Tyr	Glu	207
																								200
725	AAT	GCA	TAT	GGA	GAA	GGA	GGG	AAA	agg	TAT	GCC	TTA	TGG	GCT	GCT	AAA	ATG	GCC	CTT	TCT	CAA	AAT	ACT Thr	793 230
					Glu																			
794	GGT	GTA	CCT	TGG	ATA	ATG	TGC	CAG	CAG	TAT	GAT	GCT	CCI	GAT	CCT	GIG	ATT	GAC	ACA	TGC	TAA	TCA	TTT	862 253
231	Gly	Val	Pro	Trp	Ile	Met	Cys	Gln	Gln	Tyr	Asp	ATA	Pro	Asp	PIO	vai	TTE	ASP	1111	Cys				
863	TAC	TGC	GAC	CAA	TIT	AAA	CCA	ATC	TCT	CCA	AAC	AAG	ccc	AAA	ATT	TGG	ACA	GAG	AAC	TGG	ccc	GGA	TGG	931 276
254	Tyr	Сув	Asp	Gln	Phe	Lys	Pro	Ile	Ser	Pro	Asn	Lys	Pro	Lys	Ile	Trp	Thr	Glu	Asn	lib	Pro	GIY	TEP	270
932	JAK	DAA	ACA	Jaiah	GGG	GCC	AGA	GAT	ССТ	CAC	AGG	CCT	GCA	GAA	GAT	GTT	GCT	TAT	TCC	GTG	GCT	CGT	TTT	1000
277	Phe	Lys	Thr	Phe	Gly	Ala	Arg	Asp	Pro	His	Arg	Pro	Ala	Glu	Asp	Val	Ala	Tyr	Ser	Val	Ala	Arg	Phe	299
1001		CNA	, 333	CCA	CC A	AGC	CTC:	CAG	AAT	TAT	TAC	ATG	TAC	CAT	GGT	GGG	ACG	AAC	TTT	GGC	AGG	ACA	GCA	1069
300	Phe	Gln	Lys	Gly	Gly	Ser	Val	Gln	Asn	Tyr	Тут	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	Ala	322
1070																								1138
323	GGT	GGC	Pro	Phe	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Asp	Glu	Тут	Gly	Leu	Pro	Arg	Phe	345
																								1207
1139	CCA	AAA	TGG	GGT	CAC His	CTT	LVS	GAA	Leu	His	Lys	Val	Ile	Lys	Ser	Cys	Glu	His	Ala	Leu	Leu	Asn	Asn	368
																								1276
1208	GAT	CCA	ACT	CTT	CTT Leu	TCA	TTA	GGT	CCT	CTA	CAA Gln	GAG Glu	GCT	ASD	Val	TAT	GAA	Asp	Ala	Ser	Gly	Ala	Cys	391
																								1345
1277	GCT	GCC	TTT	CTC	GCG	AAT	ATG	GAT	GAC	AAA	TAA	GAC	AAG	GTG	GTA Val	CAG	TTC	CGA	CAT	Val	Ser	Tyr	His	414
					Ala																			
1346	TTG	CCA	GCA	TGG	TCT	GTT	AGC	ATT	TTG	CCA	GAC	TGC	AAA	AAT	GTA	GCG	TTC	AAC	ACA	GCA Ala	AAG	GTT Val	GGA Glv	1414 437
415	Leu	Pro	Ala	Trp	Ser	Val	Ser	Ile	Leu	Pro	Asp	Cys	Lys	ASI	Vai	Ala	rne	ASII	1111	<b>~</b>	DyJ	•	U-,	
1415	TGT	CAA	ACT	TCT	ATT	GTC	AAT	ATG	GCA	ccc	ATA	GAT	TTG	CAT	ccc	ACC	GCA	AGT	TCA	CCA	AAG	AGA	GAC	1483 460
438	Cys	Gln	Thr	Ser	Ile	Val	Asn	Met	Ala	Pro	Ile	Asp	Leu	His	Pro	Thr	Ala	Ser	ser	PTO	ьys	ATG	wsb	400





### 13 / 31

Figur 2
Sheet 12 of 12
Gene/clone name: TBG7/pzBG 18; accession number AF154422; Sequence ID number 7 cont.

2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAL ANG CIA GGA GAC TCC GAC GAC AAC TGT GGC ALA GGA ALA SER Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser  2588 GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT  829 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe  2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGTCATTGCCC  852 Asn Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser ***  2728 ANALYSIA DELOCATION ATTEMPT AT ACCUTTGCT ACGGGGATGCTCATTCTTTATACCAGGAAAAATCTGCTATTCCTT  2820	Gene/	clò	20 3	name	: T	BG7	/pZB	G	18	; a	CC01	ssio	n n	umbe	r J	AF15	4422	, 5	e	ce	ענ	114		•	
461 He Lys Ser Leu Gin Trp Giu Val Phe Lys Giu Thr Ala Giy Val Trp Giy Val Nak Asy Nat Try Giy Val Nak Nat Giy Try Ciy Asy Nat Try Giy Val Nak Asy Nat Giy Try Ciy Asy Nat Nat Nat Giy Try Ciy Asy Nat Nat Nat Giy Try Nat Nak Nat Giy Try Nat Nak Nat Ciy Try Nat Nak Nat Leu Phe Val Giu Ser Lys Giy Sey Nat																						_			
461 He Lys Ser Leu Gin Trp Giu Val Phe Lys Giu Thr Ala Giy Val Trp Giy Val Nak Asy Nat Try Giy Val Nak Nat Giy Try Ciy Asy Nat Try Giy Val Nak Asy Nat Giy Try Ciy Asy Nat Nat Nat Giy Try Ciy Asy Nat Nat Nat Giy Try Nat Nak Nat Giy Try Nat Nak Nat Ciy Try Nat Nak Nat Leu Phe Val Giu Ser Lys Giy Sey Nat	1484	ATC	AAG	TCT	CTT	CAG	TGG	GAA	GTC	TTC	AAG	GAA	ACA	GCT	GGA	GTA	TGG	GGA	GTT	GCT	GAT	TTC	ACT	AAA	
484 ASIN GLY PHE VEI ASP HIS 11e AST THY THY LAY ASP ALS THY ASP TYP LEW THY THY THE THE THY THE THY THE THY THE THY THE THY THE THY THY THE THY THY THY THE THY	461	Ile	Lys	Ser	Leu	Gln	Trp	Glu	Val	Phe	Lys	Glu	Thr	Ala	Gly	Val	Trp	GIY	VAI	ATA	ASP	FIIC		Lys	405
484 ASIN GLY PHE VEI ASP HIS 11e AST THY THY LAY ASP ALS THY ASP TYP LEW THY THY THE THE THY THE THY THE THY THE THY THE THY THE THY THY THE THY THY THY THE THY	1552		~~	-	CTPA	CAT	CAC	ATT	AAC	ACC	ACA	AAA	GAT	GCT	ACA	GAC	TAC	CTC	TGG	TAC	ACA	ACA	agt	TTA	
1622 TTT GTT CAT GCA GAG GAG GAT TTC CTA AGA AAC AGA GGC ACT GCA ATG CTT TTC GTT GAA TCA AAG GGT FIN Per Val His Ala Glu Glu Asp Phe Leu Arg Asn Arg Gly thr Ala Met Leu Phe Val Glu Ser Lys Gly 529 1691 CAT GCT ATG CAT GTC TTC ATC AAT AAA AAG GTT GCA GCC ACT GCA ATT GCA AAT GCC ACT GCC ACC AGG 530 His Ala Met His Val Phe Ile Asn Lys Lys Leu Gln Ala Ser Ala Ser Gly Asn Gly Thr Val Pro Gli 552 1760 TTC AAG TTT GGA ACT CCT ATT GCT CTA AAG GCA GGG AAG AAT GAA ATT TCC TTG TTA AGC ATG ACT GTG 553 Phe Lys Phe Gly Thr Pro 11e Ala Leu Lys Ala Gly Lys Asn Glu Ile Ser Leu Leu Ser Met Thr Val 575 1829 GCC CTA CAA ACA GCT GGA GCG TTT TAT GGA TGG ATT GGA GCT GGT CCA ACA AGT GTC AAA GTT GCA GGG 576 GIV Leu Gln Thr Ala Gly Ala Phe Tyr Glu Tp Ile Gly Ala Gly Pro Thr Ser Val Lys Val Ala Gly 588 1898 TTC AAG ACT GGG ACT ATG GAC TTG ATT GGA TTG GTT GCT TGG ACC TAT AAG ATT GGA GGA GAA CTT 599 Phe Lys Thr Gly Thr Met Asp Leu Thr Ala Ser Ala Trp Thr Tyr Lys Ile Gly Leu Gln Gly Glu His 621 1967 TTC AGG ATA CAG AAG TCA TAT AAC TTG AAG AGT AAA ATT TGG GCA CCA ACT TGG CAG CCA CCA AAG CAA GCG CCA CCA AAG CAA GCG CCA CCA	484	Asn	Gly	Phe	Val	Asp	His	Ile	Asn	Thr	Thr	Lys	Asp	Ala	Thr	Asp	Tyr	Leu	Trp	Tyr	Thr	Thr	Ser	Ile	506
1691 CAT GCT ATG CAT GCT TCT ATC ATC ANT ANA ANA CTT CAN GCC ACT CGA ATT GCC ACT GT ANT GCC ACT GT ANA GCA TTT GAA ACT CTT ANA GCA GGG ANG ANT GCC ACT GCA CAG GTG CCA ACT GCT ANA MAC CTT GAA ACT GCT ANA GCA GGG ANG ANT GAA ATT TCC TTC TTA AGC ATG ACT GTC STS Phe Lys Phe Gly Thr Pro 11e Ala Leu Lys Ala Gly Lys Ann Glu Tle Ser Leu Leu Ser Met Thr Val 575 1829 GCC CTA CAA ACA CCT GGA GCG TTT TAT GAA TGG ATT GGA CCT GCT CCA ACA ACT GTC AAA GTT GCA GCG GAA CAT GGA CTG GCC ACA ACA ACT GTC AAA GTT GCA GCG GAA CAT 576 1829 GCC CTA CAA ACA CCT GGA GCC TTT ATT GAA TGG ATT GGA CCT ATT ANG ATT GGA ACT GGA GGA GAA CAT 576 1829 GCC CTA CAA ACA CCT GGA CCT TTA ACT GCC GTT GCA CCT ATT ANG ATT GGA TTG CAA GGA GAA CAT 576 1829 The Lys Thr Gly Thr Met Asp Leu Thr Ala Ser Ala TTP Thr Tyr Lys 11e Gly Leu Gln Gly Glu His 52 1821 TTG AGC ATA CAG ANG TCA TAT AAC TTG AAG ATT TGG ACC CAA ACT TCG CAC CCA AAG CAA AGC ACC CCA AAG CAA GCC CCT CCT GCA CCA CCA AAG CAA GCC ACC CCT ACC ACC ACC CCA AAG CAA GCC ACC CCA AAG CAA GCC ACC CCC C																									1690
1691 CAT GCT ATG CAT GCT TTC ATC AAT AAA AAG CTT CAA GCC ACT CAA TCT GGA AAT GCC ACA CAG 530 His Ala Met His Val Phe Ile Ash Lys Lys Leu Gin Ala Ser Ala Ser Gly Ash Gly Thr Val Pro Gln 552 Phis Gly Phe Gly Phe Gly Thr Pro Ile Ash Lys Lys Leu Gin Ala Ser Ala Ser Gly Ash Gly Thr Val Pro Gl 552 Phis Gly Phe Gly Phi Pro Ile Ash Lys Ala Gly Lys Ash Glu Ile Ser Leu Leu Ser Met Thr Val 575 Fish Gly Leu Gln Thr Ala GC ATT GCA TTA GCA ATG GCA GCA GCA GCA ACA ACA ACT GCA ACA ACT ACT ACA ACA ACT GCA ACA ACT ACA ACA ACT GCA ACA ACT TCA ACA ACA ACT GCA ACA ACT ACA ACA ACT GCA ACA ACT ACA ACA ACT ACA ACA ACT ACA ACA	1622	TTT	GTT	CAT	GCA	GAG	GAG	GAT Asn	Phe	Leu	ACA	Asn	Arq	Gly	Thr	Ala	Met	Leu	Phe	Val	Glu	Ser	Lys	Gly	529
1760 TTC AAG TTT GGA ACT CCT ATT GCT CTA ANG GCA GGG AAG AAT GAA ATT TCC TTG TTA AGC ATG ACT GTG S139 Per Gly File Gly Thr Pro 11e Ala Leu Lys Ala Gly Lys Asn Glu IIe Ser Leu Leu Ser Net Thr Val 575 File Julie Gly Thr Pro 11e Ala Leu Lys Ala Gly Lys Asn Glu IIe Ser Leu Leu Ser Net Thr Val 575 Gly Leu Gln Thr Ala Gly Ala Pro Tyr Glu Trp 11e Gly Ala Gly Pro Thr Ser Val Lys Val Ala Gly 58 File Lys Tr AAG ACT GGG ACT ATG GAC TTT ATT GAA TGG ACT GGT CCA ACA AGT GTC AAA GTT GCA GGA GAA ACT 576 Gly Leu Gln Thr Ala Gly Ala Phe Tyr Glu Trp 11e Gly Ala Gly Pro Thr Ser Val Lys Val Ala Gly 58 File Lys Thr Gly Thr Net Asp Leu Thr Ala Ser Ala Trp Thr Tyr Lys 11e Gly Leu Gln Gly Glu His 621 Leu Arg 11e Gln Lys Ser Tyr Asn Leu Lys Ser Lys 11e Trp Ala Pro Thr Ser Gln Pro Pro Lys Gln 644 G16 CAG CCC CTC ACA AGG CAA ACT TTG CAG CCC CTC ACA AGG CAA ACT TTG AGG ACT ATT AAC TTG ANG AGT AAA ATT TGG CCA CCA ACT TGG CAC CTC ACA AGG CAA CTT GAT ATG 665 Gln Pro Leu Thr Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Asn Glu Pro Val Ala Leu Asp Net 666 Ile His Met Gly Lys Gly Met Ala Try Leu Asn Gly Gln Glu Ile Gly Arg Tyr Trp Pro Arg Arg Thr 691 Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 211 Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 211 Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 211 Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 211 Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 211 Gln Cys Asp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val 2311 TTA ATT ATC TTG AGG AAA ATA AGG CAA CT CAC AGG AATT GGC AGA ATT TAC ATG CAC ACA AGG CTT CCT AGG AATT GGC ACA AGG CTT CCT CAC ATG CAC ACA AGG CTT CCT CAC AGG AATT GGC CAC CAC ACA AGG CTT CCT CAC AGG AATT GGC CAC CAC ACA AGG CTT CCT CAC AGG AATT GGC CAC ACC CAC ACC AGG AATT GGC CAC CAC ACC CAC																									4.550
1760 TTC AAG TTT GGA ACT CCT ATT GCT CTA AAG GCA GGG AAG AAT GAA ATT TCC TTG TTA AGC ATG ACT GTG 1828 GGC CTA CAA ACA GCT GGA GGG TTT TAT GAA TGA ATT GGA GCT GGT CCA ACA AGT GTC AAA GTT GCA GGA 1898 TTC AAG ACT GGG ACT ATG GAC TTG ATG GAA TGG ACT GGT CCA ACA AGT GTC AAA GTT GCA 1898 TTC AAG ACT GGG ACT ATG GAC TTG ATG GAC TTG GT TGG ACC TAT AAG ATT GGA TTG CAA GGA GAA ACT 1966 TTC AAG ACT GGG ACT ATG GAC TTG ATG GAC TTG ATA AAG ATT TGG ATG CCA ACA AGT GCC AAG GAA ACA 1976 TTG AGG ATA CAG AAG TTG ATA TAC TTG AAG AGT AAA ATT TGG CCA CCA ACT TGG CAC CCA AAG CAA 1967 TTG AGG ATA CAG AAG TAT AAC TTG AAG AGT AAA ATT TGG CCA CCA ACT TGG CAC CCA AAG CAA 1968 TTC AAG ATT CAC ACA TGG TAT AAAC TTG AAG AGT AAA ATT TGG CCA CCA ACT TGG CAC CCA AAG CAA 1967 TTG AGG ATA CAG AAG TCA TAT AAC TTG AAG AGT AAAA ATT TGG CCA CCA ACT TGG CAC CCA AAG CAA 1968 TTG AAG ATG CAC ACT ATG TAT AAG CAC GTA GTA GTA GCC CCT CCT GGT AAT GAA CCT GTT GCA CTT GAT ATG 1968 TAT CAT ATG GGA AAA GGA ATG GCC TTGG TTG ATG GGC CCT CCT GGT AAT GAA CCT GTT GCA CTT GAT ATG 1968 TATT CAT ATG GGA AAA GGA ATG GCT TGG TTG ATT GGA CAA GAA ATT GGC CCG AGG AGA ACT 1968 TATT CAT ATG GGA AAA GGA ATG GCT TGG TTG ATT GGA CAA GAA ATT TGG CCG AGG AGA ACT 1971 TCC AAA TAT GGG AAA CGA ATG GCT TGG TTG ATT GAA GGA CTA TAT TAG CCT AAA TAG TAG TGT GCT ACT 1972 TAAA TAT GGG AAA CGA ATG GCT TGG TTG ATT GAA GGA CTA TAG AAG TTT TTG TAG TGG AAA TTT TGG CCG AGG AGA ACT 1973 LEU LIE TLE PHE GIU ASH CYS VAI THT GIIN CYS ASP TYT HIS VAI PYO ATG SET TTP PHE LYS PYO ATG AGT GTT TCT GGA 1973 LEU LIE TLE PHE GIU GIU ILE GIY GIY ASP PYO SET GIIN TAG TCC AAG GAA ATT GGG 1973 LEU LIE TLE PHE GIU GIU ILE GIY GIY ASP PYO SET GIIN TAG TCC AAG GAC TCC AAA ATT AGG CCA AAC CTA AGG AAA TTT 1974 CAC AGG ACA CCT CCT TCC ACT CCT TCC ACA ATT AGG TCC AAAC AGA ACT TCC GCC AAAA TTT 1975 ALB CYS GIY HIS ALSO SET VAI ASP HIS PYO SET GIIN TAG TGT GAA AAT TCC CCC GAA AAT TCC 1975 AAAC ATG CAC CTT CCT TCC ATG GAC CAC CCT CCC ACA AATT ACT CAC AGC GAA ACT TCC 1976 AAAC ATG CAC CTT TCA ATG GAC CAC CCT CCC ACA AATT	1691	CAT	GCT	ATG	САТ	GTC	TTC	ATC	TAA	AAA	AAG	CTT	CAA	GCC	AGT	GCA	TCT	GGA	TAA	GGC	ACA	GIG Val	Pro	Gln	
1829 GOC CTA CAA ACA GCT GGA GCG TTT TAT GAA TGG ATT GGA GCT GCT ACA ACT GTC CAA GGT GGA GGG 1897 1898 TTC AAG ACT GGG ACT TAG GAC TTG ACT GCT TGG ACC TAT AAG TTT GCA GGG GAA CAT 1996 TTC AAG ACT GGG ACT ATG GAT GGA CT TGT GCT TGG ACC TAT AAG ATT GGA TTG CAA GGA GAA CAT 1997 THE LLYS THE GLY THE MEL ASP LEU THE ALA SEE ALA TTP THE TY LLYS ILE GLY LEU GIN GLY GLY 1997 TTG AGG ATA CAG AAG TCA TAT AAC TTG AAG AGT AAA ATT TGG GCA CCA ACT TGC CAA GAG GAA CAT 1996 TTG AGG ATA CAG AAG TCA TAT AAC TTG AAG AGT AAA ATT TGG GCA CCA ACT TGC CAG CCA CAA AAG CAA 1996 CAG CCC CTC ACA TGG TAT AAG GCA GTA GTA GAT GAG AGT CCT CTC GGT AAT GAA CCT GTT CCA CTT GAT ATG 1906 ATT CAT ATG GGA ATA GGA ATG GCT TGG TTG AAT GGA CAA AGT GTC CAT GAT ATG 1907 ATT CAT ATG GGA ATA GGA ATG GCT TGG TTG AAT GGA CAA GAA ATT TGG CCC CTC ACA TGG TAT AAG GCA GTA GTA GAT GGA CAA GAA ATT GGC CCT CT GGT AAT GGA CAA AGA ACT 1908 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG AAT GGA CAA GAA ATT GGC CA GGA GAA ACT 1909 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG AAT GGA CAA GAA ATT GGC CAAG AGA ACT 1909 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG AAT GGA CAA GAA ATT TGG CCC AGG AGA ACT 1909 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG AAT GGA CAA GAA ATT TGG CCG AGG AGA ACT 1909 ATT CAT AAT GGG AAA CGA ATG GCT TGG TTG AAT GGA CAA GGA AAT TTT GG CCC AGA ACT 1909 ATT CAT AAT GGA AAT TGT GTT ACT CAA TGT GAC TAC AGA GGC AAA TTT AAC CCT GAT AAG TGT GCC ACT 1909 AND THE ATT GAG GAA ATA GGT TGT ACT CAA TGT GCC ACG AAA TTT AAC CCT GAT AAG TGT GCC ACT 1909 AND THE ATT ACT TGT GGT CAC CAA ACA ACA GGC AAA TTT AAC CCT GAT AAG TGT CAC 1909 AND THE AATT ATC TTT GAG GAA ATA GGT TCA GGC CAA ACT TTG TTG ATG CAA CCT ACA CAA ACA ACT ACA CAA ACA ACT ACT	530	His	Ala	Met	His	Val	Phe	Ile	Asn	Lys	Lys	Leu	Gln	ATA	ser	AIB	Ser	GIY	ASII	GIY		•••		<b></b>	
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1898 TTC AAG ACT GGG ACT ATG GAC TTG ACT GGG TCT GCT TGG ACC TATA AAG ATT GGA TTG CAA GGA CAT 1967 PHE Lys Th' Gly Th' Met Asp Leu Th' Ala Ser Ala TTP Th' Lys Ile Gly Leu Gln Gly Glu His 621 Leu Arg Ile Gln Lys Ser Tyr Ash Leu Lys Ser Lys Ile Trp Ala Pro Th' Ser Gln Pro Pro Lys Gln 644 645 Gln Pro Leu Th' Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Ash Glu Pro Val Ala Leu Asp Met 646 Gln Pro Leu Th' Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Ash Glu Pro Val Ala Leu Asp Met 647 648 Gln Pro Leu Th' Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Ash Glu Pro Val Ala Leu Asp Met 648 Gln Pro Leu Th' Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Ash Glu Pro Val Ala Leu Asp Met 649 Gln Pro Leu Th' Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Ash Glu Pro Val Ala Leu Asp Met 640 Gli Pro Leu Th' Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Ash Glu Pro Val Ala Leu Asp Met 641 Gli Pro Leu Th' Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Ash Glu Pro Val Ala Leu Asp Met 642 Leu Arg Gla AAA GGA AAA GGA ATA GGA GTA GTA GAA ATT GGA CAA GAA ATT GCC AGA ATA TTG CCC AGA AGA ACT 643 Gli Pri His Met Gly Lys Gly Met Ala Trp Leu Ash Gly Gln Glu Ile Gly Arg Tyr Trp Pro Arg Arg Thr 646 Fle His Met Gly Lys Gly Met Ala Trp Leu Ash Gly Gln Glu Tle Gly Arg Tyr Trp Pro Arg Arg Thr 647 Gly Cys Gly Glu Ash Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Ash Pro Asp Lys Cys Val Thr 748 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Ash Val 749 Cly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Ash Val 740 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 740 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Ash Leu Gln Gly Ser Glu Ile Glu 740 Ash Ara Cac Cac Cac Cac Cac Cac Cac Cac Cac Ca																									1897
1966 TTC AAG ACT GGG ACT ATG GAC TTG ACT GCG TCT GCT TGG ACC TAT AAG ATT GGA TTG CAA GGA GGA CAT 599 Phe Lys Thr Gly Thr Met Asp Leu Thr Ala Ser Ala TTP Thr Tyr Lys Ile Gly Leu Gln Gly Glu His 621 1967 TTG AGG ATA CNG AAG TCA TAT AAC TTG AAG AGT AAA ATT TGG CCA CCA ACT TCG CAG CCA CCA AAG CAA 622 Leu Arg Ile Gln Lys Ser Tyr Asn Leu Lys Ser Lys Ile TTP Ala PTO Thr Ser Gln PTO PTO Lys Gln 645 Gln PTO Leu Thr TtP Tyr Lys Ala Val Val Asp Ala PTO PTO Gly Asn Glu PTO Val Ala Leu Asp Met 667 668 TIP CL ACT ATG GTAT AAG GCA GTA GTA GTA GTA GTA GTA GTA GTA GTA GT	1829	GGC	CTA	CAA	ACA	GCT	GGA	GCG	Phe	TAT	Glu	Tro	Ile	Gly	Ala	Gly	Pro	Thr	Ser	Val	Lys	Val	Ala	Gly	598
1898 TTC AAG ACT GGG ACT ATG GAC TTG ACT GAC TO ACT OF ACT TO ACT AND GAC TTG ACT AND GAC TTG ACT AND GAC TTG ACT AND GAC TTG AGG ACT CAC AAG CAA ACT TTG AGG ACT CAC AAG CAA ACT TTG AGG ACT CAC ACT AGG CAC CAC AAG CAC CAC ACT TTG AGG ACT ACG AAG CAC CAC ACT ACG ACT ACT ACG CAC ACT ACT ACG CAC ACT ACT ACG ACT ACT ACT ACG ACT																									1066
1967 TTG AGG ATA CAG AAG TCA TAT AAC TTG AAG AGT AAA ATT TGG GCA CCA ACT TCG CAG CCA CCA AAG CAA 622 Leu Arg 11e Gln Lys Ser Tyr Asn Leu Lys Ser Lys 11e Trp Ala Pro Thr Ser Gln Pro Pro Lys Gln 644  2036 CAG CCC CTC ACA TGG TAT AAG GCA GTA GTA GTA GAT GCG CCT CCT GGT AAT GAA CCT GTT GCA CTT GAT ATG 645 Gln Pro Leu Thr Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Asn Glu Pro Val Ala Leu Asp Met 67  2105 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG ATT GGA CAA GAA ATT GCC AGA AAT TGC CCG AGG AGA ACT 668 11e His Met Gly Lys Gly Met Ala Trp Leu Asn Gly Gln Glu 11e Gly Arg Tyr Trp Pro Arg Arg Thr 690  2174 TCT AAA TAT GAG AAT TGT GTT ACT CAA TGT GAC TAC AGA GGC AAA TTT AAC CCT GAT AAG TGT GTC ACT 691 Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 713  2243 GGC TGT GGA CAA CCT ACA CAG AGA TGG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC 714 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val 736  2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TCT CAA AG GGA AAT GGC 2340  2313 TTA ATT ATC TTT GAG GAA ATA GGT GGA CAT CCA TCC TCT CAA ATT AGA TCT CAA AG GGA AAT GGC 2340  2316 CCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG 737  2450 AAC GGC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGT GAT GAA AAT CTG CAA GGA AAT TGT GAG CAA CTA AGT HIS PRO SER GLY HIS LEU SER VAL ASP HIS PRO SER PHE ASP VAL GLU ASN LEU GLN Gly Ser Glu 11e Glu 782  2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCA CCA AAT ACT AAT ATT TCC TCT GTC AAA TTT TG GAG CAA CTT GGA CAT CTA AGT TTG AAA TCT CAA ATT ATT TCC TCT GTC AAA TTT 783 ASN ASP Lys ASN Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr ASN THE SER Val Lys Phe 805  2559 GCC AGC TTT GGA AAT CCT AAT GGT ACA TTT GGC TCC TAC ATG GTA GAG AGC TCC CAC GAT CAG AAT TCT AGG GAC ACC TCG GTC GAA AAT GCT AGT TTG CTG AAC CAA AAT GGC GCA ACC TTG GTC AAA TTT TCC TCT GAG AAT TCT AGG TTG GAA ATT GCT GAG GAC TCC CAC GAT CAG GTG CAA ATT TCT CTT GGA AAT TCT CAG GTG CAA	1898	TTC	AAG	ACT	GGG	ACT	ATG	GAC	TTG	ACT	GCG	TCT	GCT	TCC	ACC	TAT	AAG	ATT	GGA	TTG	GIn.	GGA	GAA	His	
2036 CAG CCC CTC ACA TGG TAT AAG GCA GTA GTA GAT GGG CCT CCT GGT AAT GAA CCT GTT GCA CTT GAT ATG 645 GIN Pro Leu Thr Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Asn Glu Pro Val Ala Leu Asp Met 667 2105 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG ATT GGA CAA GAA ATT GGC AGA TAT TGG CCG AGG AGA ATG 668 Ile His Met Gly Lys Gly Met Ala Trp Leu Asn Gly Gln Glu Ile Gly Arg Tyr Trp Pro Arg Arg Thr 690 2174 TCT AAA TAT GAG AAT TGT GTT ACT CAA TGT GAC TAC AGA GGA AAT TT AAC CCT GAT AAG TGT GTC ACT 691 Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 713 2243 GGC TGT GGA CAA CCT ACA CAG AGA TGT GTA TAT GTG CCA CGA TCT TGG TTC AAG GCC AAA TT TAC TGT GAC ACA CAG AGA TGT TT TY HIS Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val 736 2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA 737 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 740 740 740 7416 ALA CYS Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 7416 ALA CYS Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 742 7450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCA CAC AAT ACT AAT ATT TCT CTT GTC AAAT TCT 746 ALA CYS Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 745 7450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCT CTT GTC AAAT TCT 746 ALA CYS Gly Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Tle Ser Ser Val Lys Phe 757 7580 ACC GCA CTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TCC CAC GAT CAG AAT TCT 7580 ASn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Tle Ser Ser Val Lys Phe 7581 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TCC CAC GAT CAG AAT TCT 7580 ALA CAC CTG GTC GAA AAG GTT TCC CTG AAC GAA AAT GCT AAT GGA AAT CTC CAC GTA AAC TTT 7581 ASN ASP Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Thr Ca CC CAC GAT CAC TTT																									
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2036 CAG CCC CTC ACA TGG TAT AAG GCA GTA GTA GAT GGG CCT CCT GGT AAT GAA CCT GTT GCA CTT GAT ATG 645 Gln Pro Leu Thr Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Asn Glu Pro Val Ala Leu Asp Met 667  2105 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG ATG GAC CAA GAA ATT GGC AGA TAT TGG CCG AGG AGA ACT 668 Ile His Met Gly Lys Gly Met Ala Trp Leu Asn Gly Gln Glu Ile Gly Arg Tyr Trp Pro Arg Arg Thr 690  2174 TCT AAA TAT GAG AAT TGT GTT ACT CAA TGT GAC TAC AGA GGC AAA TTT AAC CCT GAT AAG TGT GTC ACT 691 Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 713  2243 GGC TGT GGA CAA CCT ACA CAG AGA TGG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC 714 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val 736  2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA 737 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 759  2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GAA AGT GAA ATT GAG 760 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 782  2450 AAC GAC AAA AAC AGG CCA ACT CTA ACT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT 783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Tla Ser Val Lys Phe 806 Ala Ser Phe Gly Asn Pro Asn GJT TGC CTG AAC TGT GGT TCC TAC ATG CGA CTG CAC GAA ATT TCC TGT CAAA TTT 783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Tla GAA ATG TCC AGC GAA AAT TCT 826 GAA AAC TGT GAA AAT CTT AAA TTT TCC TCT GTC AAA TTT 783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Tle Ser Val Lys Phe 806 Ala Ser Phe Gly Asn Pro Asn GJT TAC CTG AAC TGT GAA CTG CAC GAA ATT TCC TCT GAA ATT TCC TCT GAA AAT TCT GAA GAA ATG TCC AGC GAA AAT TCT 826 GAA AAC TGT GAA AAT GTT GAA AAT GTC AAA TGT GAA ATT TCC TCT GAA AAA GTT TCC CTG AAA AAG GTT TAC CTG AAA AAA GAG TTT CAA GGA GAA ATG TCC AAC GAA AAA GTT TCC CTG AAA AAA GTT TCC AAA GAT	622	Leu	Arg	Ile	Gln	Lys	ser	Tyr	Asn	Leu	Lys	Ser	Lys	Ile	Trp	Ala	Pro	Thr	Ser	Gln	Pro	Pro	Lys	GIn	644
2105 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG AAT GGA CAA GAA ATT GGC AGA TAT TGG CCG AGG AGA ACT G68 Ile His Met Gly Lys Gly Met Ala Trp Leu Asn Gly Gln Glu Ile Gly Arg Tyr Trp Pro Arg Arg Thr 690 C714 TCT AAA TAT GAG AAT TGT GTT ACT CAA TGT GAC TAC AGA GGC AAA TTT AAC CCT GAT AAG TGT GTC ACT G11 Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 713 C243 GGC TGT GGA CAA CCT ACA CAG AGA TGG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC 714 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val 737 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 759 C737 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 759 C760 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 782 C450 AAC GAC AAA AAC GCC CAA ACT CAA AAT ACT AAA ACT CAC AGA AAT TCT CT GTC AAA TTT 763 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 2518 GCC AGC CTT GAA CTC TAC ATG GGA CAC CTC TAC ATG CTA AAT ACT AAA ATT TCC TCT GTC AAA TTT 763 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 2519 GCC AGC TTC GAA AAG GCT ACA TGC TAC ACT GAC TAC ATG CTA GAA ATT CTC TCT GTC AAA TTCT 6806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser 828 GCA GCA CTC GAC GAT CCA ACT AAT ACT AAA TCT CAC GCA AAC TCT CAC GCA AAC ACT TCT GTC GAA CTG GAC GCA CTG GTC GAA AAG GTT TCC CTG AAC CAA AAT GAG TTA GAA ATG CCA GCA AAC TTC AGC GCA CTG GAC GAC GAC CTG GAC GAC GAC GAC GAC GAC GAC GAC GAC GA																									2104
2115 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG AAT GGA CAA GAA ATT GGC AGA TAT TGG CCG AGG AGA ACT 668 Ile His Met Gly Lys Gly Met Ala Trp Leu Asn Gly Gln Glu Ile Gly Arg Tyr Trp Pro Arg Arg Thr 690 2174 TCT AAA TAT GAG AAT TGT GTT ACT CAA TGT GAC TAC AGA GGC AAA TTT AAC CCT GAT AAG TGT GTC ACT 691 Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 2243 GGC TGT GGA CAA CCT ACA CAG AGA TG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC 714 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val 716 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val 717 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 718 CCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA AGG AAG GTT TCT GGA 718 ASN ASP Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 719 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG GGA GAC TGC CAC GAT CAG AAT TCT 719 ANA ASP Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 725 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT 725 GCA AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT 726 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser 726 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Gln CTG GAC TGT GAA ATT TCC AGC GCA AAC TTT 726 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAC TTG GAC GTT GAA GTG AAT TCC AGC GCA AAC TTT 727 AAA ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TCC AGC GCA AAC TTT 727 AAA ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TCC AGC GCA AAC TTT 727 AAAATGAAATGACAATATCTAATTTTAAAGATATGAGTTCTATATTATAACCATTCACACAGATAAACCTTCTTATATAACCATTCACACAGATAAACTTTCATATTCATTTTGAAAGATATTCATTTTAAAACATTATTTAT	2036	CAG	CCC	CTC	ACA	TGG	TAT	Lvs	Ala	Val	Val	Asp	Ala	Pro	Pro	Gly	Asn	Glu	Pro	Val	Ala	Leu	Asp	Met	667
2105 ATT CAT ATG GGA AAA GGA ATG GCT TGG THG ATG GAG GAG GAG AAA TTG AGG CAG AAA AGG CT TCG AGG AAA TGC CTG TAG AATG AGG AAA AGG CT TCG AGG AAA AGG CT TCAG AGG AAA AAC AGG CAG CAG CAG CAC CAC																									2173
2174 TCT AAA TAT GAG AAT TGT GTT ACT CAA TGT GAC TAC AGA GGC AAA TTT AAC CCT GAT AAG TGT GTC ACT 691 Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr 713  2243 GGC TGT GGA CAA CCT ACA CAG AGA TGG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC 714 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val 736  2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA 737 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 759  2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TCT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG 760 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 782  2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT 783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 805  2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT 806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser 82588 GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT 8257 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGCATTGCCC 852 AAA ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGCATTGCCC 852 AAA ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGCATTGCCC 852 AAA ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGCATTGCCC 852 AAAA TGT CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGCATTGCCC 852 AAAA TTG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGCATTGCCC 852 AAAA TGT CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGCATTGCCT 852 AAAATGAATGAATATCTAATTTTAATATGTTTGCTACGGAGAGATGCTCATTCTTTATTAAACCTTTCTTT	2105	TTA	CAT	ATG	GGA	AAA	GGA	ATG	CCT	TGG	TTG	TAA	GGA	CAA	GAA	TIA	GGC	AGA	TAT	Tro	Pro	Arg	Arg	Thr	
2241 GGC TGT GGA CAA CCT ACA CAG AGA TGG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC  7.14 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val  7.36  2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA  7.37 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly  7.59  2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG  7.60 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu  2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT  7.83 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe  2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT  806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser  2587 BCS GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT  829 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe  2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TCC AGC TGA GTGCACTTGCCC  852 ASN Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser  2729 AAAATGAATGAACTATTCTAATTTTATATGAGTTGCTGAGGGGAGTGCTCATTCTTTATATAGCAGGAAAAATTTCATGTTTGAAAGACTAA  2912  2729 AAAATGAATGAACTATTCTAATTTTATATGAGTTGCTGAGGGGAGTGCTCATTCTTTATATAGCAGGAAAAATCTGCTATTCCTT  2820  2728 AAAATGAATGAACTATTCTAATTTTATATGAGTTTCCTAGGGGGGATGCTCATTCTTTATATAGCAGGAAAAATCTGCTTATTTGAAAGACTAAA  2912  2729 AAAATGAATGAACTATTCTAATTTTATATGAGTTTCCTAGGGGGAGTGCTCTATTCTTTATATAGCAGGAAAAATCTTGCTTTTTGAAAGACTTAACCTTTCTTT																									
2241 GGC TGT GGA CAA CCT ACA CAG AGA TGG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC  7.14 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val  7.36  2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA  7.37 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly  7.59  2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG  7.60 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu  2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT  7.83 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe  2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT  806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser  2587 BCS GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT  829 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe  2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TCC AGC TGA GTGCACTTGCCC  852 ASN Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser  2729 AAAATGAATGAACTATTCTAATTTTATATGAGTTGCTGAGGGGAGTGCTCATTCTTTATATAGCAGGAAAAATTTCATGTTTGAAAGACTAA  2912  2729 AAAATGAATGAACTATTCTAATTTTATATGAGTTGCTGAGGGGAGTGCTCATTCTTTATATAGCAGGAAAAATCTGCTATTCCTT  2820  2728 AAAATGAATGAACTATTCTAATTTTATATGAGTTTCCTAGGGGGGATGCTCATTCTTTATATAGCAGGAAAAATCTGCTTATTTGAAAGACTAAA  2912  2729 AAAATGAATGAACTATTCTAATTTTATATGAGTTTCCTAGGGGGAGTGCTCTATTCTTTATATAGCAGGAAAAATCTTGCTTTTTGAAAGACTTAACCTTTCTTT	2174	TCT	AAA	TAT	GAG	AAT	TGT	GTT	ACT	CAA	TGT	GAC	TAC	AGA	GGC	AAA	LalaL	AAC	CCT	GAT	AAG	TGT	GTC	ACT	
2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA 737 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG 760 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT 783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT 806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser 2587 AAC ATG CAA TG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA ATT TCC AGC GCA AAC TTT 8529 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe 2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TCC AGC TGA GTGTCATTGCCC 2728 852 Asn Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser 2729 AAAATGAATGACATATTCTAAGTTTAAGTTTGCTACGGAGATGCTCATTCTTATAAGCCATCACCAGATAAACCTTTGATATACGTAGATTTCATAGATTATCTAAGATTATCTAAGGATATTGCATAGATTACTTAAGGATATTGCATAGATTACATTTGAAAGATTATCTAAGGATATTGCATAGATTACTTAAGGATATTGCATAGATTACTTAAGGATATTGCATAGATTACATTTTAAAGATTATCTAAGGATATTGCATAGATTACTTAAGGATATTCATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATATTCAATGTTTGAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATT	691	Ser	Lys	Tyr	Glu	Asn	Cys	Val	Thr	Gln	Cys	Asp	Tyr	Arg	Gly	Lys	Phe	Asn	Pro	Asp	Lys	Cys	vaı	TILL	713
2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA 737 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly 2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG 760 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT 783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT 806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser 2587 AAC ATG CAA TG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA ATT TCC AGC GCA AAC TTT 8529 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe 2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TCC AGC TGA GTGTCATTGCCC 2728 852 Asn Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser 2729 AAAATGAATGACATATTCTAAGTTTAAGTTTGCTACGGAGATGCTCATTCTTATAAGCCATCACCAGATAAACCTTTGATATACGTAGATTTCATAGATTATCTAAGATTATCTAAGGATATTGCATAGATTACTTAAGGATATTGCATAGATTACATTTGAAAGATTATCTAAGGATATTGCATAGATTACTTAAGGATATTGCATAGATTACTTAAGGATATTGCATAGATTACATTTTAAAGATTATCTAAGGATATTGCATAGATTACTTAAGGATATTCATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATATTCAATGTTTGAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATT					~~~	~~	NC N	CNG	) AGA	TCC	тат	САТ	GTG	CCA	CGA	TCT	TGG	TTC	AAG	CCA	TCA	GGA	AAT	GTC	
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2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG 760 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu 2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT 783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT 806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser 2588 GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT 8258 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe 2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGTCATTGCCC 852 ASN Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser 2728 AAAATGAATGACATATTCTAATTTTATATGGTTTGCTACGGAGATGCTCATTCTTTATAGCCATTATCTTGGATATTCATGTTTGAAAGACTAA																									2380
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2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAT AAT CTG CAG GAG AAT TCT 760 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu  2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT 783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe 805  2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT 806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser 828  2588 GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT 829 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe 851  2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGTCATTGCCC 872  852 Asn Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser ****  2729 AAAATGAATGACATATTCTAACTTTATATAGGTTTGCTACGGAGATGCTCATTCTTATAAGCCATTCATT																									2440
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2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TAC CCC ALA AAT ACT ATT ACT TTG TAC TTG AAA TAC TAC ATT ACT ACT TTG AAA TAC TAC TAC ATT ACT TTG AAA TAC TAC TAC ATT ACT TTG AAA TAC TAC TAC ACT ACT ACT ACT ACT ACT	760	Ala	Cys	Gly	His	Leu	Ser	Val	Asp	His	Pro	Ser	Phe	Asp	Val	. GIU	Asn	Leu	GIn	GIY	Ser	GIL	*16		,
2587 AAA ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC GTG AAT TGC AGC AAT TGT AAG ATA GTT AAA GTA AAG AAA CTT GCA GTT GAA AT GTT AAG ATA GTT AAA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC GTA AAC TTT 2656 AAC ATG CAA ATG CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT 2656 AAC ATG CAA ATG CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT 2656 AAC ATG CAA ATG CAA ATG GTG CAA ATG TGC AGC TGA AAT AAA AAT GAG TGT GAA GTG AAT TGC AGC TGA GTGTCATTGCCC 2728 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGTCATTGCCC 2728 ASA Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser ***  2729 AAAATGAATGAACATATTCTAATTTTATATAGTTTGCTACGGAGATGCTCATTCTTAAACCTTTCTTATATAGCAGAAAAATCTGCTATTCCTT 2820 CTTTTCTTATATAGATGATGAATGAATGAATGAATGAATTTAAAGATTAAGATTATAGGTATTCCTTATATAAGCATTATCATGTTTGAAAGACTAA 2912	2450					NCC	. ~~	ъст	СТА	AGT	TTG	AAA	TGC	ccc	ACA	AAT	ACT	AAT	ATT	TCC	TCT	GTC	AAA	TTT	
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2588 GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT 829 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe 2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGTCATTGCCC 852 ASN Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser *** 2729 AAAATGAACATATTCTAATTTTATATAGGTTTGCTACGGAGATGCTCATTCTTTAAACCTTTCTTATATAGCAGAAAAATCTGCTATTCCTT 2820 CTTTTCTTATATGATTTGAAGTTTTGAAGATTATGAGTTACTGATTCTTTATATAAGCATTAACCTTTGGATATTCATGTTTGAAAGACTAA																									2587
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2588 GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG ICC AGC TGA GTG GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG ICC AGC TGA GTGCATTGCCC  2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGCATTGCCC  852 ASA Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser ***  2729 AAAATGAATGACATATTCTAATTTATATAGGTTTGCTACGGAGATGCTCATTCTTATAACCTTTCTTATATAGCAGAAAAATCTGCTATTCCTT  2820 2821 CTTTYCTCTATGATTTGAAGGTTTAAGATTATGAGTACTGATGCTTTATTAAGCATCACCAGATAACCTTTGGATATTCATGTTTGAAAGACTAA																									2656
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852 Asn Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Ash Cys Sel  2729 AAAATGAACATATTCTAATTTATATAGTTTGCTACGGAGATGCTCATTCTTAAACCTTTCTTATATAGCAGAAAAATCTGCTATTCCTT  2820 2821 CTTTCTTCTATGATTTCTAAGATATCAGATATCAGTTACTGATTCTTTATTAAGCATCACCAGATAACCTTTGGATATTCATGTTTGAAAGACTAA	265	7 222	י אחי	2 CA		ייביאף ב	, CC2	AGT	ACA	GTA	AAG	AAA	CTI	GCA	GM	GAA 1	GTG	TAA	TGC	AGC	TGA	GTG	TCAT	TGCC	2728
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TBG1-ORF		-24			MGFWMA	MUMILLELW	VSCGISVSYD	26
TBG2-ORF		-14		MCRRKT	INFPLILIVL	TIHFVIVAGE	ALKELMALIN	36
TBG3-ORF					MCCTLILMIN	VLUVLLGSWV	FSGTASVSTU	30 28
TBG4-ORF		-22		• • • • • • • • •	MLRINVLL	LIVICILDEE	SSVKASKSED	50
TBG5-ORF		_						50
TBG6-ORF		1	MNTMSCLSS	NEW EVET A CT	VTWMTVMSSS	LAAVDASNVT	TIGTOSVTYD	49
TBG7-ORF					MOUGTOTHW	SHAMESCLE	SWISHSIA	29
apple carnation		-21		MT.CC	KENNVMKMMI	VYVFVEITLI	SCAAGNAMATI	34
asparagus					MY ISK4-Y/ I:MIFW	VARIEMAVWOR		30
broccoli					MKMKQFNLLS	<b>IFLIEITSFG</b>	SANSTIVSHD	30 38
Lupin		-12		MEGSRIVM	ESIMSRRNFH	WATERTALAMA	CX MANNEY THE	36
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			60 HKÄTTVNGOR	VTIGEOGRAV	DD CODE MADE	Vəbəsikəliki	DVFOTWAWN	76
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TBG2-ORF		~ 4	THE PARTY OF THE P	DATE OF COME	PRSTPEMWPG	IIOKAKEGGV	PATCHE EXTENS	. 80
TBG3-ORF TBG4-ORF		29	DRATITINGKR	KILISCSIHY	PRSTROMWPD	LIOKAKDGGL	DVJETVALOW	78
TBG5-ORF		51						100 100
TBG6-ORF		51		morning matrices	STORES AND STATES		EXECUTE ON	99
TBG7-ORF		50	RRSLTINGOR	KLMSASTRY	PRSVPAMVEG	LIDEANTSCH		79 -
apple		20		BARRIE TO THE PARTY OF THE PART	EKS PERMIT	ITERASDSOL		84
carnation		35	YRATK INDOR HKSV TINGOR		PRSTIPEMMED	LECKAKOGGL	DUECTYVEVIN	80
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TBG1-ORF		77	GHEDETECKAA	<b>EEE KADIAKA</b>	BKVVCEAGEX	VIII BASHSAN	A FOR COMM	136
TBG2-ORF		87	GHERIRGOW	SECULIAR DE	AKINGSHGIP			130
TBG3-ORF		81	GHEROOGIANA			Will Control	A SWARE OF SWARE	128
TBG4-ORF		79	CHEST CKYN	FERKENINE	VKINERAGIF	VHIREBYC	AEWAY GENEL	150
TBG5-ORF TBG6-ORF		101	VIESTONIN	GER	VETTEKE	ANTERVE		150
TBG7-ORF		100	CHESTONY	FCCTF PINCE	CKITCONIME	MILETERYA	<b>建加度于</b> 区	149
apple		80	GHEPSPGNYY	DE ROPE	HANGEGIF	VNERTGRAVO		129 134
carnation		85	GHE ESEGKYY	ERGERA PHYSIC	TOVINI PROMUZIE	VILLEGELAC	474441941410055555555	130
asparagus		81	GHEPSPGQYY.	GGRYDLIRE	PRINK GURA	SVIRIGPYVO	AEWNY GGEPV	130
broccoli		81	AHEPSRRQYD GHEPSPGKYY	PEDELLER	TRIMONGIF	VHIRIGPFIC	AEWNEGGEPV	138
Lupin		89	GHEPSPGKIL	PENT DESIGNATION	*********	• <del>                                     </del>	7	
			160	170	180	190	200	
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TBG2-ORF			TOTE	DOMESTA DESKUESE	MERYVKKAND	LMISE	PEDMEGGET	186 180
TBG3-ORF			· · · · · · · · · · · · · · · · · · ·	DIMERY DESCAR	MOKETIA KIVN	MMKAE	KTIFIAGGET	178
TBG4-ORF		129	WLKYVPGMEF	RINNOPEKVA	MOGENOKEVN	MTKSE	NT YASOGGPV	200
TBG5-ORF		151	WLHFIPGIEF WLKYVPGISF	PA DATE DERVIA	WKCAV EKLINI INVIETNITAD	LMKIITESSL	RVVOSYSHRL	200
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TBG7-ORF			FRENCTAE	DUIDATEDEVAA	MOKETEKIVS	MMKAE	KINDIOGGET	179
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broccoli			CH TRACTORNO D	DULLING EMME	MONFTIKLVN	WWKEE	PITTAGGGTT	188
Lupin		139	WLKYVPGIAF	RTDNEPFKEA	WOKETEKIVN	IMKAE	KTHOSOGGET	100
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TBG1-ORF		- 0-	THE A TENTER	CNIURCSEC	PKCKLYMKWA	ALMAVGIGAG	A BMA MATACLA T	236
TBG2-ORF			TT CO TENTEY	CDMEWELG	APGKSYAOWA	AKMAVGLLUIG	A BMA MCVOD	230
TBG3-ORF TBG4-ORF		100	TO A TENEV	CDVEWETC	APCKAYTKWA	AOMAVGLECIG	A PARTITUDE -	228
TBG5-ORF		001	TEATEV	CARCITECTYC	PRAKPYVNWA	ASMATSLNIG	VPWVMCQQ-P	250
TBG6-ORF		201	MACHACI VDDV	TORHELI	STORGLOIWO	LDLNIG	VPWVMCKEE-	250 249
TBG7-ORF		200	TT CO MENTEY	GVVENAVG	FCCKRYALWA	AKMALSUNIG	ABMTMC-CO:	229
apple		100	TT CO TENTET	GPVEWEIG	APCKAYTKWA	AOMAVGLDIG	ALMINCKOF-	234
carnation		185	ILNO-IENEY	GPVEWEIG	APGKAY'IHWA	<b>WOLING STIME</b>	A PARTICUÓRO	





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TBG1-ORF TBG2-ORF TBG3-ORF TBG4-ORF TBG5-ORF TBG7-ORF apple carnation asparagus broccoli Lupin		277 287 281 279 301 300 280 285 281	310 MEAVAREL DEFALARIT LESVARIV MEAVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT LAYSVARIT	320 OTGESEINYY ORGESLONYY OKGESEINYY ONNGSEENYY OKGESVONYY OKGESVONYY OKGESVONYY OKGESPANYY OKGESPANYY OKGESPANYY OKGESPANYY OKGESPANYY OKGESPANYY OKGESPANYY OKGESPANYY	MYREGINETS	340 PSCHOOL PARTY PSCHOOL PART	350 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	326 336 330 328 350 350 349 329 334 330 330 338
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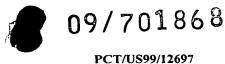
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TBG6-ORF		451				E:	VODEN OF OFF	499
TBG7-ORF		450	VAFNTĀKVĢC	QTSIVNMAP-		EHPIASSE	KKDIKSDUME	479
apple								
carnation								484
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asparagus								480
broccoli		431	EAYMTARVNT EVFNTAKVNS	DDI RDK		MTP	VNSAFAWQ	488
Lupin		439	EAL MINITAL AND	PRIMIT— A.S.		, , , , , ,		
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TBG2-ORF		487	S-FNEDAASH T-LKEPLGVW	CDKN-ÉÄZKÖ	TOPHTWATER	Oppiaming	ALLOCOE-RE	530
TBG3-ORF								528
TBG4-ORF	•	479	S-YNEETPTA	DDSDILTANG	IMEOKNATIRE	SSDATMAMIN	MATASIAE- GE	
TBG5-ORF		501						550
								550
TBG6-ORF	•				FVDHENTEKE	BTHYLWYTTS	IFVHAEE-DE	549
TBG7-ORF		400	V-FKETAGVW S-FIEETITSS S-YSDEVPTA	Service DG	TYPOTHI THE	TTEXHWYMIA	ITIGSDR-AR	529
apple		480	2-27 5537 43	DCDC44ABEKK	GWEMEE FOR VE	KSTYLWYMID	WILDGNE-GE	534
carnation		485	A-YTÉDTDAL	ATTAL OFFICE	ENTRIES STUDIES	RSHVIWYTTY	VDIAKNE-EË	530
asparagus		481	A-YTEDTDAL	MIN- MARKETS	THE TOTAL PROPERTY.		WHI.DKKDPIW	530
broccoli		481	PERLIOKLIL	KGSGDLIANS	HADOVD ATTACK	COMPANY OF	WATGPAD	538
Lupin		489	S-YNEEPASS	SENDPVŁGYA	TAM GRACE ASSERTS	20133330351133	AVI WALL AND	
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TBG1-ORF		527	INSEN-MINI	TVFSASHALH	NEW ACCIDENCE.	AN SERVINGS	ARCONOT GINER	
TBG2-ORF			TOTAL TEN SE TRAIN	TTTCMPDFT/R	THATAXAGUAC	AKGKWT	VAAGE Mirtha	586
				ATT NACTOR STREET, TAXABLE	THE TRUE COLUMN ( THE	ANICHTER PRIM	TO STATE OF THE ST	580
TBG3-ORF		227	TKNCK-DEAT	HIVITAGANATA	VEVNGKISGT	VYGILENPKI	TY SCHVKLEA	<b>57</b> 8
TBG4-ORF		529	Tiviain Deni	MARCHARITY CO.	7,00007			<b>60</b> 0
TBG5-ORF								600
TBG6-ORF			LRN-RGTAME		TOT TWY TO A C	SE ENCTY FOR	KEGTPIAEKA	599
TBG7-ORF		550	IRN-RGIAME	I VE SKODALIO	THE AMERICAN	UNESTENDED!	SESONUNLES	579
apple		530	TKNGK-SELL	TIT SAGDATA		WALL TO BE	TIMESON BROWN	584
carnation		535	LKKGD-EPWE	TAN SAGHVE	VANGOTO E		MACCENTINE	580
asparagus		531	LRN-RGTAML LKNGK-SPLL LKKGD-EPWI LKTGK-YPYL	TVMSAGHAVH	AET NGG PECT	AYISSIRAVENIA	AT SOSHVING	580
broccoli								588
Lupin		539	IKDCK-MEATE	TAMSACHVIN	ATT MANA TOTAL	BYPSINDERIK	ATTENDED ATTAINED	200
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		E77	610 GVNKISIJEI GYNDILIIESE GVNKISIIESI	AUGUPNVGPH	<b>FETWINAGVISG</b>	EVSINGINE	nRDLTWQ	626
TBG1-ORF		5//	CONTRACTOR OF THE SEC	TVICEONYGAE	LEKDGAISFKG	OIKERGCKSG	DINLTIS	636
TBG2-ORF		28/	CINDALITATION OF THE CIT	AVICTION GPH	FETWNAGVIG	PUSLITGIDEG	KRDETWQ	630
TBG3-ORF		281	GUNKISLLSV	COLUMN COLUMN	VIVININGVIG	PATTI SGLNEG	SRNLAKO	628
TBG4-ORF		579	GINKISHISV.	2 A GITETA A SA 11				650
TBG5-ORF		601						650
TBG6-ORF		601			100 MONOR	CONTRACTOR	mMDITAS	649
TBG7-ORF		600	GKNE ISLLSM	TVGLQUAGAL	YE-WIGAGPI	SYNVAGENIG	m tattime (3a)	629
apple			ACCRECATE A PARTY	עיובו אומי דייו אי	FETWINAC VIII	PITTRELASE	TAATT-TOCAL	634
carnation			CONTRACTOR OF THE PROPERTY CONTRACTOR OF THE PRO	HIMEOTON A. TENTO	FERVIX	PARTICIPATION	T	630
asparagus			CONTRACT COTT. CO.	ווועבוניוואכו וביניבי	THUMBULL	RANDALINER	V	630
broccoli			CONTRACT & T.Y.CT.		FESCIPICING	PAKENGIKUD	E I TEMÉTICA	
		589	GNNKISLLSV	SVGLANVGTH	FETWNTGVLG	PVTLTGLSSG	TWDESKQ	638
Lupin		307	C 1111	£ 15.5				
			660	670	680	690	700	
			· · · · · · · · · · · · · · · · · · ·	ENT OF HOUSE	SPSVEWVE	GSLVAOKOPL	SWYKTTFNAP	676
TBG1-ORF		627	LWTYQVGLRG	CATTOTATION OF	TECAC-TATE	POTCHTOCAL	SWYKTKFDAP	686
TBG2-ORF		637	LWTYQVGLRG KWSYKVGLKG	EF LEVYDVINS	TESUG-MIE	CCLANODODI	TWYKSTENAP	680
TBG3-ORF		631	KWSYKVGLKG	EALSTHSTISG	SSSVEWVE	GSDVAQAQED	TENVEN TENIA D	678
TBG4-ORF		629	KWSYKVGLKG	ESLSLHSLSG	SSSVEWVK	POSTATIONOLOGIC	THILLESTER	700
TBG5-ORF								700
TBG6-ORF								
TBG7-ORF				せいしゅうしゅうしゅう	TKSKTWAP	TSOPPKOOPL	TMIKWAAADWE	699
				EXTAINMENTS	SSSVEWVE	GPSMALKUPL	TMINUTION	679
apple			· · · · · · · · · · · · · · · · · · ·	エゼンへてアントラスに	SCHOOWGP	PAWKOPL	OMITITEDAT	684
carnation			TOTAL TOTAL	COUNTY OF MOTOR	SSNVFWGE	. A5 UNUPL	TMINILITARE	680
asparagus	3	631	OMDAKIGING KMLAÖTGING	ENTRY I DEMINIO	VCHHIDKMG	FKI PADRM-I	SWYKANFKAP	680
broccoli	,	631	QWDYKIGING KWSYKIGLKG	LIMIN TR PLINS	POINTING MOT	CSLYVAKKUDI	AWYKTTFSAP	688
Lupin		639	KWSYKIGLKG	ESLSLHTEAG	31/2 A ₽ M A Å	SOLVERINGED		
-					m- ^	740	750	
			710	720	730	740		726
TBG1-ORF		677	710 DGNEPLALDM	NTMGKGQVWI	NGQSLGRHWP	AYKSS-GSCS	A-CMATGMED	720
		•						





DNASIS Multiple	edit1			Figure Sheet				
TBG2-ORF		687	GGTDEVALLE	SSMCKGOAWV	NEHHVGRYWT	LVAPN-NGO	RTOPERGARH	
TBG3-ORF				A THE PROPERTY OF THE PARTY.	MEGCI CIRVUD	CVKAC-CUCT	A - GARRISME M	
TBG4-ORF		CTO	COMPANY NO FOL	ACMICKEOTHI	NGEGVGRHWP	GYLAU-GDGS	V-CD KNOTLIA	
TBG5-ORF		701	Periodicinal Property of the Periodical Property					
TBG6-ORF		701	PGNEPVÄLEM		MARTCHVID	PPTCKVFNÖN	TOČOVRCKEN	
IBG7-ORF				COMPONITION	Manayarhwe	GYTAR-GSG	D-COINCIID	
apple		680	GGNDPLALDL	CEMERCOAWT	NOOSTGRHWS	NNTAK-GSCN	DNCNYAGTYT	
carnation		C01	DOMESTIC DESCRIPTION	NTIMESKEEOT WIL	NCOSIGRYWP	AYKAS-GSCG	2-CDXKGTXN	
asparagus			T COLONIA COLONIA	AND CHECK TANK	MAGGICKAMB	SFNSSDEGGT	EECDIKGEIG	
oroccoli Lupin		689	AGNOPLALDL	GSMGKGEVWV	NGOSIGRHWP	GNKAR-GNOG	N-CNYAGTYT	
orban.								
			760	770	780	790	800	,
TBG1-ORF		727	EKKCLINGGE	GSORWYHVPR	SMIX LIGNT	V-VFEEWGGD	PLOTITION OF	
TBG2-ORF		737	SDKCRINGGE	TTOAWYHI PR	SWIKTLNIVL	V-IFEETDKI	Protestation	
TBG3-ORF		731	EKKCLENGGE EKKOMWOO	ASORWXHYPR		V. J. S.	DIGITAL RE	
TBG4-ORF		729	EKKCONNCAO	ESTERNATOR OF THE	OWWEN A SAME	AL SHARMAN	#** HENDEMAKE - FORD	
PBG5-ORF								
TBG6-ORF		750	PDKCZVIG ČČĆO	PTORWYHYPR	STEETS COVE	I-IFEEIGED	PSO TRESMEK	
TBG7-ORF apple		730	DKKCRTHCGE	PSORWYHI PR	MIST PICANTA	V-VEEEWASD	RSRISDVERG	
carnation		735	ETKCL SDCGK	SSOKWYHVIE	BMO PROMIE	A-ALEEMOND	TKWVSIVKHT	
asparagus		731	PDKCVTGCGO DKKCRTHCGE ETKCLSDGCK EKKCLSDGCB SDKCAFMGCK DTKCLANGSO	ASORWYHVER	BART STONE P	R-NT BENESIS	PIGIEMVKRS	
broccoli		731	SDKCAFMCGK	PTORWYHYPE	SFINDKCHNT	ITLEEEMGGU	PSMVKFKTVV	
Lupin		739	DTKCTANG90	PSORWYHVER	<b>SME</b> GG GAA F	AL AL ETHAPS	Bindiiv Date Gr	
				820	830	840	850	
		777	810 IGSVÇADÎYÊ	ACE CONTRACTOR CONTRACTOR		THE PROPERTY OF	GTOODTH CCT	- ;
TBG1-ORF		707	IGSVCAULYE TETI CAOVSE VASVCAUINE	KHYRPIHKWS	HSEFDRKLSL	MDKTPEMHIQ	CDECHTESSI	
TBG2-ORF TBG3-ORF		781	VASVCADINE	WO-POLVIWO	MOBSCKVEKP	IRPKAHIS	CASGOKOTT ST	
TBG4-ORF		779	EM-2ACMENTAR					
TBG5-ORF								
TBG6-ORF		801	VSGACGHLSV		~~~~~			
TBG7-ORF		800	VSGACGHLSV	-DHRSFDV	ENLOGSEIEN	DKNREITLSEK	CPININESSV	
apple		780	IA VASVCAEVEE		TA	m		
carnation		785	IA	TO TOWN	my five	-b PKVHIS	CDPGOKMSKI	
asparagus								
broccoli		787	TGRVCAKAHE					
Lupin		,05						
			860	870	880	890	900	
TBG1-ORF		827	KFASFGTPEG	VCGNFQQGSC	HAPRSYDAFK	KNCVG	RESUSVOVIP	
TBG2-ORF		837	EFASYGSPNG	SCOKESOGKC	HAANSLSV	VSQACIG	VISCRIGITAL	
TBG3-ORF		831	KFASFGTPQG	VCGSFREGSC	HATHSIDATE	RICIG	QNSCSVEVIE	
TBG4-ORF								
TBG5-ORF		051						
TBG6-ORF		827	KFASFGNPNG	WOODWI COC	HYDNIGATIVE	KVCLN	ONECALEMSS	
TBG7-ORF apple		920						
apple carnation		025						
asparagus		021	ALES GEOGRAPOOC	TYTESTERS	HAHKSYDAFE	OEGLMONCVG	OEFCSVNVAP	
broccoli		001	THE OTHER PROPERTY.	OCCUPANCE.	FC AKDAVKV-	VAKECVG	KLINCIMINVSS	
Lupin		839	KFASEGNESG					
				000	930	940	950	
		0==	910 ENFGGDP-CR	920	730 TCS			
TBG1-ORF		877	ENFGGDP-CR GVFG-DP-CR	MATIVITY AND	KCSPPPDI ST	SASS		
TBG2-ORF		001	THE POOR OR	LITAMICET STATES	TCS			
TBG3-ORF								
TBG4-ORF TBG5-ORF		001						
TBG5-ORF		001						
TBG7-ORF		000	ANTENDACT - CD	CHYNKKI AVJEV	NCS			
				KT				
apple								
apple carnation		885						
		001	EVFGGDP-CP HKFGSNLDCG	CTMKKT.AVEA	TCE			





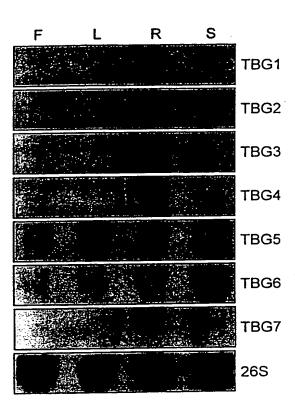


Figure 4. Autoradiograph of northern blot analysis of TBG expression in various plant tissues. Twenty µg of total RNA extracted from flowers (F), leaves (L), roots (R) and stems (S) was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown.







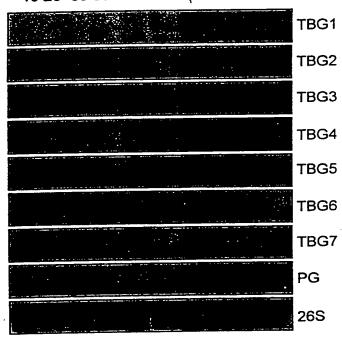


Figure 5. Autoradiograph of northern blot analysis of TBG expression in fruit tissues. Twenty µg of total RNA extracted from peel and outer pericarp tissue was loaded in each lane. Fruit were harvested at 10, 20, 30, 35, and 40 days postpollenation and at the breaker (Br), turning (Tr), pink (Pk), red (Rd) and over ripe (OR) stages. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control.





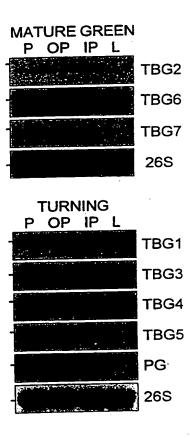


Figure 6. Autoradiograph of northern blot analysis of TBG expression in fruit tissues. Twenty  $\mu g$  of total RNA extracted from mature green or turning stage fruit peel (P), outer pericarp (OP), inner pericarp (IP) and locular (L) tissue was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control.





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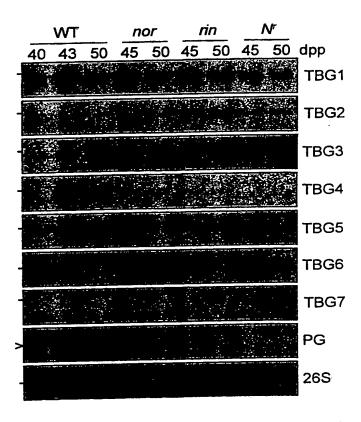


Figure 7. Autoradiograph of northern blot analysis of TBG expression in normal and mutant fruit tissues. Twenty µg of total RNA extracted from peel and outer pericarp tissue at various days post-pollination (dpp) was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control. The - and > marks on the left indicate the position of the tomato 27S and 18S rRNAs respectively.

EN IL ILI M. ILD ILI

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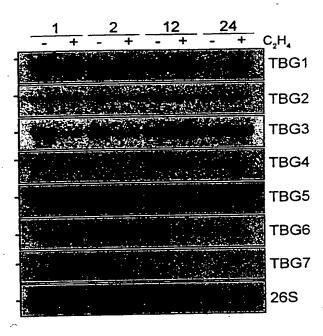


Figure 8. Autoradiograph of northern blot analysis of TBG expression in response to ethylene treatment of mature green fruit tissues. Twenty μg of total RNA extracted from peel and outer pericarp tissue at various times (1, 2, 12 and 24 hours) after treatment with (+) or without (-) 10 ppm ethylene was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. The - marks on the left indicate the position of the tomato 27S rRNA.

M III

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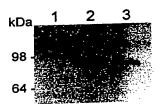
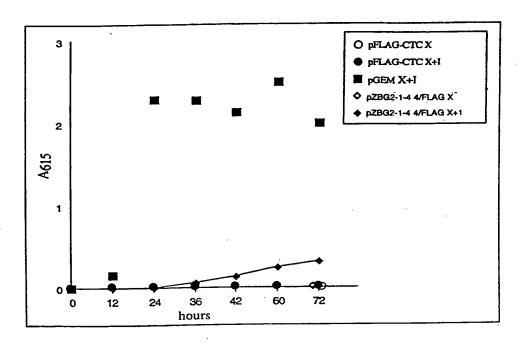


Figure 9. Western blot analysis of TBG4 expression by yeast. A yeast clone was isolated that secreted high levels of FLAG-TBG4 fusion protein into the culture medium. Protein samples were separated in an 8% acrylamide gel, transferred to nitrocellulose and were blotted with M1 anti-FLAG primary antibody. Blots were washed and blotted with an alkaline-phosphatase conjugated secondary antibody and alkaline phosphatase activity was detected using Sigma Fast substrate. Lane 1, culture medium of an untransformed yeast clone was used as a negative control. Lane 2, culture medium of yeast clone expressing FLAG-TBG4 fusion protein. Lane 3, Affinity purified FLAG-TBG4 fusion protein.

24 / 31

Figure 10





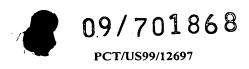
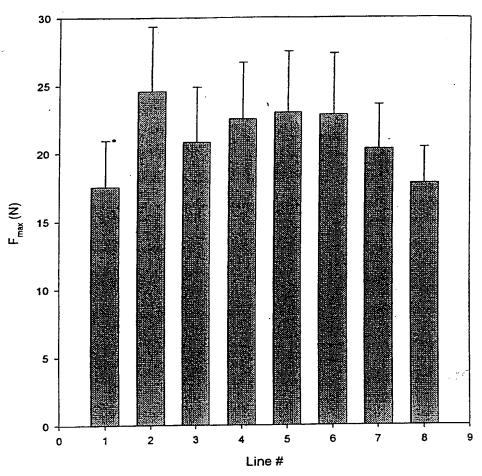


Figure 11A

### Flat plate compression to 3 mm Breaker + 7 d



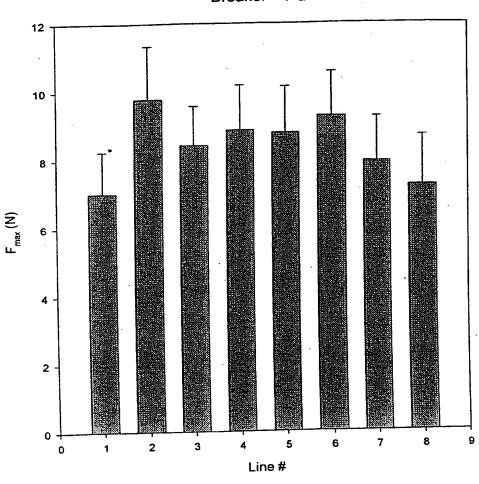
#### Standard Deviation

FP07 Line #FP07 mean FP07 std dev

	,	
1	17.52665	3.418542
2	24.56026	4.786548
3	20.81681	4.066194
4.	22.54655	4.15923
5	23.03255	4.493091
6	22.84338	4.517462
7	20.36124	3.24608
8	17.81924	2.665468



Figure 11B
Spherical indentor to 3 mm
Breaker + 7 d



Standard Deviation

SP07 Line #SP07 Mean SP07 Std Dev

	111000.	
1	7.02	1.22
5	9.77	1.57
6	8.43	1.15
7	8.87	1.32
8	8.78	1.36
9	9.28	1.29
11	7.96	1.30
12	7.26	1.45



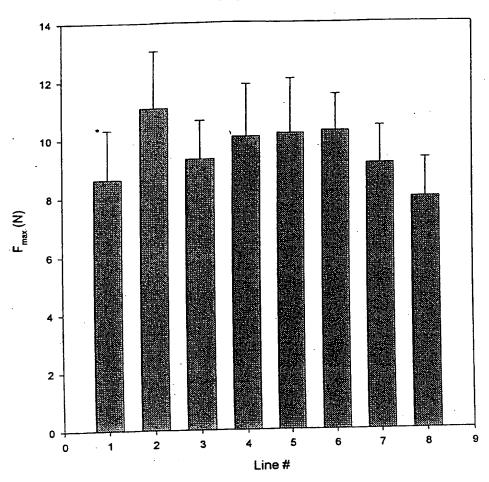


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Figure 11C

## 4-mm cylindrical indentor-to mm. Breaker + 7 d



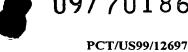
Standard Deviation

## CY07 LINE#CY07 Mean CY07 Std Dev

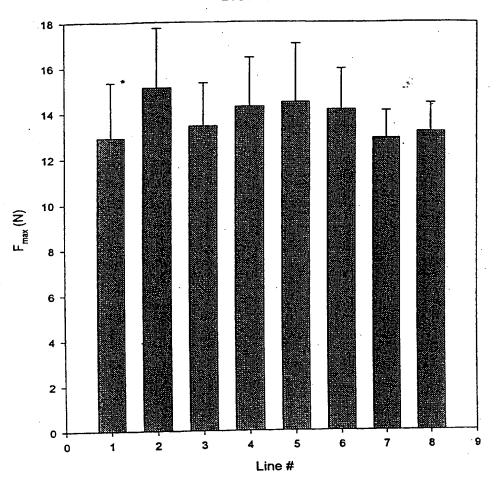
1	8.62	1.69
5	11.07	1.96
6	9.31	1.33
7	10.07	1.81
8	10.18	1.88
9	10.27	1.26
11	9.15	1.30
12	7. <b>9</b> 9	1.33



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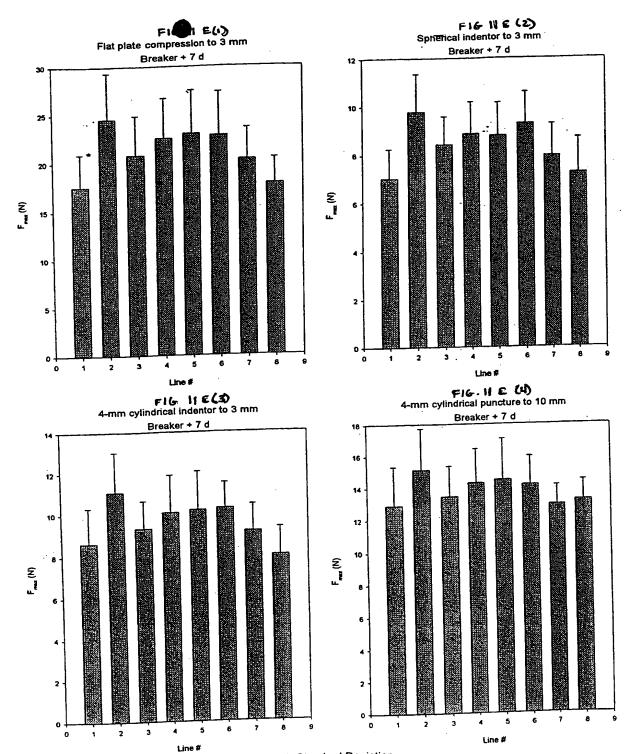




### Standard Deviation

PU07 Line# PI	U07 Mean PL	107 Std Dev
1	12.91	2.43
5	15.13	2.61
6	13.44	1.90
7	14.28	2.16
8	14.47	2.58
9	14.14	1.81
11	12.90	1.20
12	13.18	1.25





Standard Deviation

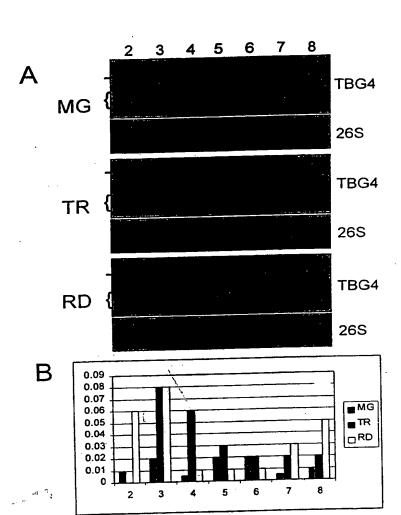


Figure 12. Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct. A. Total RNA was extracted from mature green/42 days post-pollenation (MG), turning/breaker + 3 (TR) and red/breaker + 7 (RD) fruit and twenty μg was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control. The marks - and { denote the positions of the endogenous TBG4 and antisense mRNAs respectively. Lanes 2-8 correspond to transgenic lines 2-8 in Figures 11A-E. B. Chart of TBG4 mRNA levels in lines 2-8. Autoradiographs were scanned using a densitometer and TBG4 mRNA levels were corrected against the loading controls. TBG4 mRNA levels are shown in arbitrary units.

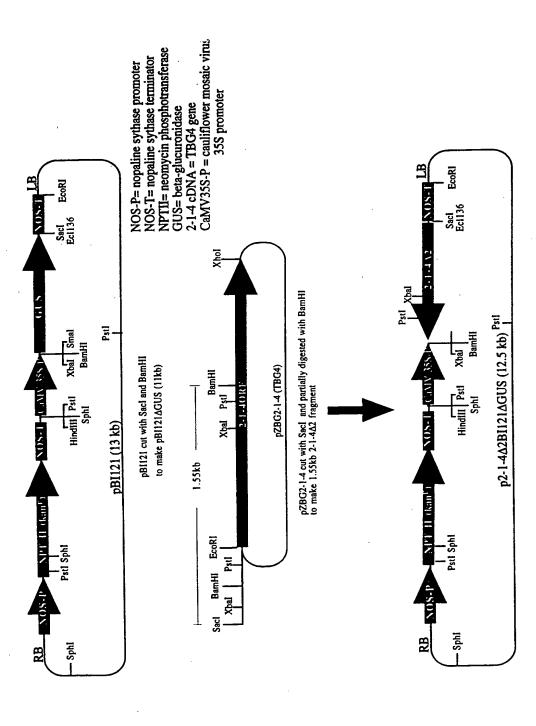


Figure 13. Binary construct used to transform plants and express TBG4 (pZBG2-1-4) in the antisense orientation.